

STE20_h	MAH	LRGFANQH	SRV	---	DPEELFTKL	DRIGKGSFGEV	YKGI	NDN	HTK	43																															
MST3_h	MAH	SPVQSGLP	GMQNLK	ADPEELFTKL	EKIGKGSFGEV	FKGI	NDN	RTQ	47																																
STLK2_h	MAH	SPVAVQVP	GMQNNIA	DPEELFTKL	ERIGKGSFGEV	FKGI	NDN	RTQ	47																																
STLK3_h	TAAPAA	PAPAPAPAA	QAAGWPI	CRDAYELQ	EVI	SGATAVV	QAAL	CKPRQ	57																																
STE20_h	EVVAIK	IIDLEAE	DEIEDIQ	QEITVLS	QCDSPI	ITRYFGSYLK	STKL	WII	MEYLG	100																															
MST3_h	KVVAIK	IIDLEAE	DEIEDIQ	QEITVLS	QCDSPI	TKYYGSYLK	DTKL	WII	MEYLG	104																															
STLK2_h	QVVAIK	IIDLEAE	DEIEDIQ	QEITVLS	QCDSPI	TKYYGSYLK	GSKL	WII	MEYLG	104																															
STLK3_h	ERVAIK	RINLEK	CQTSMD	ELLKEIQ	AMSQC	SHPNV	VV	YTS	FVKDEL	WLV	IMKLL	SG	114																												
STE20_h	GSALD	LLKPGP	---	LEET	YIA	TILREIL	KGLDYLH	SER	KI	HRDI	KAA	NVLL	148																												
MST3_h	GSALD	LLKPGP	---	LDET	QIA	TILREIL	KGLDYLH	SEK	KI	HRDI	KAA	NVLL	152																												
STLK2_h	GSALD	LLRAGP	---	FDEF	QIA	TILKEIL	KGLDYLH	SEK	KI	HRDI	KAA	NVLL	152																												
STLK3_h	GSMLD	IIK	YIVNR	GEH	KNGV	LEEA	IIATIL	KEV	LEGLDYLH	RNGQ	IHRDL	KAGN	ITLL	171																											
STLK4_h	---	---	---	KSGV	L	D	X	STIA	TILREV	LEGL	EYLH	KXGQ	IHRD	V	KAGN	ITLL	X	41																							
STE20_h	SEQG	DV	VKL	ADFGV	-A	---	GQL	TD	TQ	I	KRNT	FV	GT	PF	WM	A	PEV	I	KQ	SA	-	YDF	K	ADI	198																
MST3_h	SEHG	E	VKL	ADFGV	-A	---	GQL	TD	TQ	I	KRNT	FV	GT	PF	WM	A	PEV	I	KQ	SA	-	YDS	K	ADI	202																
STLK2_h	SEQG	DV	VKL	ADFGV	-A	---	GQL	TD	TQ	I	KRNT	FV	GT	PF	WM	A	PEV	I	KQ	SA	-	YDS	K	ADI	202																
STLK3_h	GEDG	SV	Q	IA	DFGV	SA	FL	AT	G	GD	V	TR	NKV	-R	K	T	F	V	GT	P	C	W	M	A	P	E	V	M	E	Q	V	R	G	Y	D	F	K	A	D	M	227
STLK4_h	GEDG	SV	Q	IA	DFGV	SA	FL	AT	G	GD	I	TR	NKV	-R	K	T	F	V	GT	P	C	W	M	A	P	E	V	M	E	Q	V	R	G	Y	D	F	K	A	D	I	97

Fig. 1A

Fig. 1B

STE20_h	RQ--PRSQCLSTLVRPVFGELKEKHKQSGGSGVGALEELENAFSLAEESCPGISDKLM	405
MST3_h	IPKRPFSQLSTIISPLFAELKESQACGGNLSIEELRGAIYLAEEACPGISDTMV	411
STLK2_h	-----CLSMIITPAFAELKQQDENNASRNQAIIEELKSI AVAAACPGITDKMV	400
STLK3_h	DY--REASSCAVNVLRLRNSRKELNDIRFEFTPGRDTADGVSSQELFSAGLVDGHDV	468
STLK4_h	-----ISLVLRLRNSKELNDIRFEFTPGRDTAEGVSSQELISAGLVDGRDL	366
STE20_h	VHILVERVQRFSHNRRNHLTSTR	426
MST3_h	AQLVQRLQRYSLSGGGTSSH	431
STLK2_h	KKLIEKFQKCSADESP	416
STLK3_h	VIVAAANLQKIVDDPKALKTLTFKLASGCDGSEIPDEVKLIGFAQLSVS	516
STLK4_h	VIVAAANLQKIVEEPQSNR[VTFKLASGVEGSDIPDDGKLIGFAQLSIS	414

Fig. 1C

Ste20_h	MAHLRGFANQHSRV	----	DPEELFTKLDRI	IGKGSFGEVYK	GIDNHTK	43		
T19A5.2_ce	MTTSSDELPRQADD	SMKWDRIYIQKLD	PEVIFTKQERIG	SGFGEVYK	GIDNRTG	57		
Pak_sp	-----	-----	LLYRNFVKIGQ	SGASGDVY	SARQVGIN	26		
STLK5_h	-----	-----	-----	-----	-----	0		
Ste20_h	EVVAIKIIDL	EEAEDIED	IQQEI	TVLSQCDS	PIYTRYFGSYLK	STKLEWIIIMEYLG	100	
T19A5.2_ce	RVVAIKIIDL	EEAEDIED	IQQEI	QVLSQCDS	QYVTKYFGSFLK	SGSKLWIIIMEYLG	114	
Pak_sp	LSVAIKKMNIN	QPKKEF-IIVNEI	LV	LMKSHHKN	IVNFIDTFFYK	SELWMVMEYMRG	82	
STLK5_h	-----	-----	-----	-----	-----	-----	0	
Ste20_h	GSALDLLKPG	PLEET	YIA	TILREI	LKGLDYLH	SERKIH	RDIKANV	157
T19A5.2_ce	GSALDLTKSG	KLDESHIA	VILREI	LKGLEYLH	SERKIH	RDIKANV	VLVSEHGDV	171
Pak_sp	GS	LTEVVTNNTL	SEGGIAA	ICKET	LEGLQLHL	HENGIV	HRDIKSDN	139
STLK5_h	--LIC	THFMDGMNELA	IAYIL	QGV	LKALDY	IHHM	GYVHR	55
Ste20_h	DFGVAGQL	TD	TIKRNT	TFVGT	PF	-----	WMAPEV	205
T19A5.2_ce	DFGVAGQL	TD	TIKRNT	TFVGT	PF	-----	WMAPEL	219
Pak_sp	DFGFCAQ	IDSNMT	KRTT	IMVGT	TPY	-----	WMAPEV	187
STLK5_h	GLRSNLS	MISAGQRQR	VVHDF	PKYS	VKVL	PWLSPEV	LQNLQGYDAK	112
Ste20_h	IELAKGEPP	NSDLHP	MRV	LF	FLIPK	-NSPP	TLEG-Q	238
T19A5.2_ce	IELANGEP	PHSD	LHPMRV	LV	FLIPK	-NPP	PVLQGSQ	253
Pak_sp	IELMVEGE	PPYLNEN	PLRALY	L	IATIGT	PKISR	PEL	222
STLK5_h	IELANGHVP	FKDMPA	TQM	LEKLN	-GTV	PC	LLD-TSTIPAEEL	167
							TMSPSR	
							SVANSGLS	

Fig. 2A

Fig. 2B

ZC504.4_ce	MSSSGEDE---	IDLNSLRDPAGIFEL	IEVVNGTYGQVYK	GRHVKT	AQLAAIKIMNINE	58	
NIK_m	MANDSPAKSLVD	IDLSSLRDPAGIFEL	VEVVNGTYGQVYK	GRHVKT	VT-AAIKVMDVTE	69	
ZC1_h	MANDSPAKSLVD	IDLSSLRDPAGIFEL	VEVVNGTYGQVYK	GRHVKT	TGQLAAIKVMDVTE	60	
ZC2_h	-----	-----	AFGEVYEGRHVKT	TGQLAAIKVMDVTG	-----	28	
ZC3_h	-----	-----	AFGEVYEGRHVKT	TGQLAAIKVMDVTE	-----	28	
ZC504.4_ce	DEEIDEIKLEINMLKKHSHHRN	VATYYGAFIKKL	PSSTGKH	DQLWLVMEFCGS	GSITDLVK	116	
NIK_m	DEEEETLEINMLKKYSHHRN	IATYYGAFIKKSPPGHD	---	DQLWLVMEFCGAGS	ITDLVK	117	
ZC1_h	DEEEIKLEINMLKKYSHHRN	IATYYGAFIKKSPPGHD	---	DQLWLVMEFCGAGS	ITDLVK	118	
ZC2_h	DEEEIKQLEINMLKKYSHHRN	IATYYGAFIKKPPGMD	---	DQLWLVMEFCGAGS	VTDLIK	84	
ZC3_h	DEEEIKQLEINMLKKYSHHRN	IATYYGAFIKKSPPGND	---	DQLWLVMEFCGAGS	VTDLVK	84	
ZC504.4_ce	NTKGGSLLKEEWIAIYICREILRGLYHLHQ	SKVIHRDIKQNVLLT	DSAEVKLVDF	FGVSAQL		176	
NIK_m	NTKGNTLKEDWIAIYSREILRGLAHLHI	HHVVIHRDIKQNVLLT	ENAEVKLVDF	FGVSAQL		177	
ZC1_h	NTKGNTLKEDWIAIYSREILRGLAHLHI	HHVVIHRDIKQNVLLT	ENAEVKLVDF	FGVSAQL		178	
ZC2_h	NTKGNTLKEDWIAIYICREILRGLSHLHQ	HKVVIHRDIKQNVLLT	ENAEVKLVDF	FGVSAQL		144	
ZC3_h	NTKGNAALKEDCIAIYICREILRGLAHLHA	HKVVIHRDIKQNVLLT	ENAEVKLVDF	FGVSAQL		144	
ZC504.4_ce	DKTVGRRNTFIGTPYWMapeVIAcDES	PEATYDS	RSRLWSL	GITAL	EMAEGHPPLCDMHP	236	
NIK_m	DRTVGRRNTFIGTPYWMapeVIAcDEN	PDATYDYRSD	LWSC	CGITAI	EMAEGGPPPLCDMHP	237	
ZC1_h	DRTVGRRNTFIGTPYWMapeVIAcDEN	PDATYDYRSD	LWSC	CGITAI	EMAEGAPPLCDMHP	238	
ZC2_h	DRTVGRRNTFIGTPYWMapeVIAcDEN	PDATYD	FKSD	LWSL	GITAI	EMAEGAPPLCDMHP	204
ZC3_h	DRTVGRRNTFIGTPYWMapeVIAcDEN	PDATYDYRSD	TW	SLGITAI	EMAEGAPPLCDMHP	204	

Fig. 3A

ZC504.4_ce	MRALFLIPRNPPPPKILKRNNKKWTKKFFETFFIETVVLVKDYHQRPYTGALLRHHPFFIKEQPHEQT	296
NIK_m	MRALFLIPRNPPPPRLK-SKKWSKKFFSFIEGCLVKKNYMQRPSTEQLLKHPPFIRDQPNERQ	296
ZC1_h	MRALFLIPRNPPPPRLK-SKKWSKKFFSFIEGCLVKKNYMQRPSTEQLLKHPPFIRDQPNERQ	297
ZC2_h	MRALFLIPRNPPAPRLK-SKKWSKKFFSFIESCLVKKNHSSQRPATTEQLMKHPPFIRDQPNERQ	263
ZC3_h	MRALFLIPRNPPPPRLK-SKKWSKKFTDFIDTCLIKTYLSRPPTEQLLKFPPFIRDQPTTERQ	263
ZC504.4_ce	IRHSIKEHIDRNRVRVKKQDADYEYSGSEDDIEPSPNNRRDSESS--SMIPMDNTLRKGFQ	353
NIK_m	VRIQLKDHIDRTRKKRGEKDETEYEYSGSEEEEEVEPEQEGEPSSIVNVPGESTLRRDFL	356
ZC1_h	VRIQLKDHIDRTRKKRGEKDETEYEYSGSEEEEEVEPEQEGEPSSIVNVPGESTLRRDFL	357
ZC2_h	VRIQLKDHIDRTRKKRGEKDETEYEYSGSEEEEEVEPEQEGEPSSIVNVPGESTLRRDFL	321
ZC3_h	VRIQLKDHIDRTRKKRGEKDETEYEYSGS-EEEDDSHGEGEPSSIMNVPGESTLRRDFL	322
ZC504.4_ce	KLQESSRGFAEPGAQQLRRLPQQPAPAPFYQQSRYVEPRRESSSEVKLRAVSSRGAADGP	413
NIK_m	RLQQENKSEALRRQQLLQEQQL-----REQEEYKQQLLAERQKRI--	398
ZC1_h	RLQQENKSEALRRQQLLQEQQL-----REQEEYKQQLLAERQKRI--	399
ZC2_h	RLQLANKSEALRRQQLLQEQQL-----RENEEHKQQLLAERQKRI--	361
ZC3_h	RLQQENKSNSEALKQQQQLQQQQQ-----RQPEAHIKHLHQRRRI--	364
ZC504.4_ce	RHSPASRPRPRSPQQSHPAAPHLADLANYEKRRRSEREERRERERQAHHAMPIARVSA SV	473
NIK_m	EEQKEQRRRLEEQQRREREARRQQEREQRRRIEEKRRLEELERRRKEEEERRRRAEEEEKR	458
ZC1_h	EEQKEQRRRLEEQQRREREARRQQEREQRRRIEEKRRLEELERRRKEEEERRRRAEEEEKR	459
ZC2_h	EEQKEQRRRLEEQQRREREKELRKQQRREHYEEQMR-----FEERR	404
ZC3_h	EEQKFERRRVEEQQRREEREQRKLQEKEQRRLEDMQAL-----RREERR	409

Fig. 3B

ZC504.4_ce	PAPQQSRKMSEPLILITHVKPEEDLDVLA S ELSKIMGG	508
NIK_m	RVEREQEYIRRQLEEEERHLETLQQQLLQEAMLL	493
ZC1_h	RVEREQEYIRRQLEEEERHLEVLQQQLLQEAMLL	519
ZC2_h	RAEHQEQYKIRKQLEEQ	435
ZC3_h	QAREEQEYIRHRLEEEERQLEILQQQLLQEALLL	469
ZC504.4_ce	HHNGRISREES-MSPPPPAPPPPREASISSITDIDVGELDNGAQA EWDDLKDIMM	561
NIK_m	HDHRRIPHAQ-QQPPPPQQQDRSKPSFHAPFEPKPHYDPADRAREVIQWSHLASLKN	548
ZC1_h	YLLSLQHDHRRIPHPQHSSQPPPPQQQERSKPSFHAPFEPKAHYEPADRAREVEDRFRKTNHS	579
ZC2_h	YLLVSLQHQR	484
ZC3_h	YLLKSLQQQQQQLQK-QQQQLLPQDRKPLHYHGRGMNPADKPAWAREVERTRMKNKQQ	528
ZC504.4_ce	NGEGTLRG	595
NIK_m	NYSPVSRSHSFSDPSPKFAHHHLRSQDPCPPSRSEGLSQSSDSKSEVPPEPTQK	599
ZC1_h	SPEAQSKQ	620
ZC2_h	SPAMPHKV	531
ZC3_h	NSPLAKSK	574
ZC504.4_ce		595
NIK_m		599
ZC1_h		620
ZC2_h	LVAVKSQGPALTASQSV	575
ZC3_h	KSLVAHRVPLKPYAAPVPRSQSLQDQPTRNLAAFPASHDPDPAIPAPTATPSARGAVIRQ	634

Fig. 3C

ZC504.4_ce
-----NSGHGAYKGGKIPERIRPGIISL-DDDDSD 623
NIK_m
-----AWSRSDSEVPVPRVVRTTSRSPVLSRRDSPQLQGGGQNS 639
ZC1_h
-----PQVPVRTTSRSPVLSRRDSPQLQ-GSGQQN 648
ZC2_h
NSDPTSENPLPTRIEKFRSSWLRQEEDIPPKVPQRTTISISPAIARKNSPGNGSALGPR 635
ZC3_h
NSDPTSEGPGSPNPP-----AWVRPD-NEAPPKVPQRTSSIAATALNTSGAGGSRPAQAVR 689

ZC504.4_ce
SDNE-----EGNEPLMFKPIVRCPFISFFWFLS-- 651
NIK_m
QAGQ-----RNSTSSIEPRLLWERVEKLVP[RP]G-- 667
ZC1_h
SQAG-----QRNSTSIEPRLLWERVEKLVP[RP]G-- 676
ZC2_h
LGSQ-----PIRASNPDLRRTEPILESP[LR]TS[SG] 665
ZC3_h
ARPRNSAWQIYLQRRRAERGTPKPPGPAQPPGPPNASNPDLRRSDPG-----WERS-- 742

ZC504.4_ce
--ANVIHSVDGSIPLVKHLIWFQNASSSRRGALPDLLPKSPCLRRQINDQTRQMSDDRADE 709
NIK_m
--SGSSSGSSNSGSGQPGSNPGSQSGSGERFRVRSSSKSEGGSPSPRQESAAKKPDDKKEVF 725
ZC1_h
--SGSSSGSSNSGSGQPGSNPGSQSGSGERFRVRSSSKSEGGSPSPRQESAAKKPDDKKEVF 734
ZC2_h
SSSSSTPSSQPSQSGSQSGSQAGSSERTRVRANSSKSEGGSPVLPHEPAKVKPEESRDIT 725
ZC3_h
--DSVLPA[SH]GHP-----QAGSLERNRVGVSSKIPDSSPVLSPGNKA[KP]DDHRSRPG 792

ZC504.4_ce
Q[PN]GFGQ-----NSDSR-----SSIQHSFSNRDREK[SF]VG[VF]GGGAGAGGGTVNRPG--- 755
NIK_m
RSLKPA[GEV]-----DLTAL-----AKELRAVEDVRPPH[KVT]DYSSSSEESGTTDEEEEDV[ED] 777
ZC1_h
RPLKPA-----DLTAL-----AKELRAVEDVRPPH[KVT]DYSSSSEESGTTDEEEEDV[EQ] 783
ZC2_h
RPSRPA[SYKKA]IDEDLTALAKELRELRIEETNRPM[KKVT]DYSSSSEESSESSEEEEDGES 785
ZC3_h
RPA[DFV]-----L-----LKERTLDEAPRPPK[KAM]DYSSSSEEVESSEDD[EE]EGEG 837

Fig. 3D

ZC504.4_ce
NIK_m
ZC1_h
ZC2_h
ZC3_h
755

EGADDS TSGPEDTRAASSPNLSNGETESVKTMIVHDDVSEEPAMTP--SKEGTLIV-- 831
EGADES TSGPEDTRAASSNLNSNGETESVKTMIVHDDVSEEPAMTP--SKEGTLIV-- 837
ETHDGTVAVSDIPRLIPTGAPGSNEQYNVGMVGTTHGLETSHADSFSGISREGTLMIRET 845
GPAEGS--RDTPGGRDGDTSVSTMVVHDVEEITGTQPP--YGGGTMVVQRT 885

ZC504.4_ce
NIK_m
ZC1_h
ZC2_h
ZC3_h
755

SGEKRS GHS DSN GFAGHINLPDLVQQSHSPAGTPT EGLGRVSTHSQEMDSSGTEYGMGSS 905
PEEERNLLHADSNGYT--NLPDVVQPSHSPTENSKGQSPPSKDGSGDYQS RGLVKAPG- 941

ZC504.4_ce
NIK_m
ZC1_h
ZC2_h
ZC3_h
ZC4_h
772

SSSFTPFIDPRLLQIISPS SGTTVTSVVGFS CDGLRPEAIRQDPT--NQVQVNVTPN SN 772
SSSFTPFIDPRLLQIISPS SGTTVTSVVGFS CDGM RPEAIRQDPT--RKGSVNVVNPT 901
TKASFTPFVDP RVYQTSP TDEDEE DESSAALFTGELLRQEAKLNEARKISVNVVNPT 965
-KSSFTMFVDLGIYQPGGSGDSIPITALVGGEGTRL DQLQYDV--RKGSVNVVNPT 994
--NPNPL 5

ZC504.4_ce
NIK_m
ZC1_h
ZC2_h
ZC3_h
ZC4_h
832

GTPAENDAPEIRKYKKKFSGEILCAALWGVNLLIGTDSGLMLLDRSGQ GK VYPLISRRRF 832
NTRPQSDTPEIRKYKKRNFSEILCAALWGVNLLVGTESGLMLLDRSGQ GK VYPLISRRRF 961
NTRPQSDTPEIRKYKKRNFSEILCAALWGVNLLVGTESGLMLLDRSGQ GK VYPLINRRRF 967
NIRPHSDTPEIRKYKKRNFSEILCAALWGVNLLVGTENGLMLLDRSGQ GK YYNLINRRRF 1025
NTRAHS ETPEIRKYKKRNFSEILCAALWGVNLLVGTENGLMLLDRSGQ GK VYGLIGRRRF 1054
YVSPACKKPLIHMYEKEFTSEICCGSLWGVNLLIGTRSNLYLMDRSGKADITKLI RRRPFE 65

Fig. 3E

ZC504.4_ce	DQM	TV	LEG	Q	N	I	L	A	T	I	S	G	R	K	R	R	I	R	V	Y	Y	L	S	W	L	R	Q	K	I	L	R	T	E	G	A	G	S	A	N	T	T	E	K	R	N	G	W	V	N	V	G	D	--	889						
NIK_m	QQ	MD	V	LEG	N	V	L	V	T	I	S	G	K	K	D	K	L	R	V	Y	Y	L	S	W	L	R	N	K	I	L	H	N	D	P	E	V	--	--	--	--	--	--	--	--	--	--	--	--	--	1013										
ZC1_h	QQ	MD	V	LEG	N	V	L	V	T	I	S	G	K	K	D	K	L	R	V	Y	Y	L	S	W	L	R	N	K	I	L	H	N	D	P	E	V	--	--	--	--	--	--	--	--	--	--	--	--	1019											
ZC2_h	QQ	MD	V	LEG	N	V	L	V	T	I	S	G	K	K	N	K	L	R	V	Y	Y	L	S	W	L	R	N	R	I	L	H	N	D	P	E	V	--	--	--	--	--	--	--	--	--	--	--	--	1077											
ZC3_h	QQ	MD	V	LEG	N	V	L	V	T	I	S	G	K	R	N	K	L	R	V	Y	Y	L	S	W	L	R	N	K	I	L	H	N	D	P	E	V	--	--	--	--	--	--	--	--	--	--	--	--	1106											
ZC4_h	RQ	L	Q	V	L	E	P	L	N	L	I	T	I	S	G	H	K	N	R	L	R	V	Y	H	L	T	W	L	R	N	K	I	L	N	D	P	E	S	--	--	--	--	--	--	--	--	--	--	120											
ZC504.4_ce	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	944												
NIK_m	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	1068												
ZC1_h	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	1074												
ZC2_h	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	1132												
ZC3_h	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	1161												
ZC4_h	KA	ID	K	L	T	G	C	E	H	F	S	V	L	Q	H	E	E	T	Y	I	A	I	A	L	K	S	S	I	H	L	Y	A	W	A	P	K	S	F	D	E	S	T	A	I	K	V	E	P	T	L	D	H	K	P	V	T	V	180		
ZC504.4_ce	DL	T	V	E	D	N	A	R	L	K	V	L	Y	G	S	T	G	F	H	A	I	D	L	D	S	A	A	V	Y	D	I	Y	T	P	A	Q	S	G	Q	T	T	I	P	H	C	I	V	V	L	P	N	S	N	G	M	Q	L	L	1004	
NIK_m	DL	T	V	E	E	G	Q	R	L	K	V	I	Y	G	S	C	A	G	F	H	A	V	D	V	D	S	G	S	V	Y	D	I	Y	L	P	T	H	I	Q	C	S	I	K	P	H	A	I	I	L	P	N	T	D	G	M	E	L	L	1128	
ZC1_h	DL	T	V	E	E	G	Q	R	L	K	V	I	Y	G	S	C	A	G	F	H	A	V	D	V	D	S	G	S	V	Y	D	I	Y	L	P	T	H	I	Q	C	S	I	K	P	H	A	I	I	L	P	N	T	D	G	M	E	L	L	1134	
ZC2_h	DL	T	V	E	E	G	Q	R	L	K	V	I	F	G	S	T	G	F	H	V	I	D	V	D	S	G	N	S	Y	D	I	Y	T	P	S	H	I	Q	G	N	I	T	P	H	A	I	V	I	L	P	K	T	D	G	M	E	M	L	1192	
ZC3_h	DL	T	V	E	E	G	Q	R	L	K	V	I	Y	G	S	S	A	G	F	H	A	V	D	V	D	S	G	N	S	Y	D	I	Y	I	P	V	H	I	Q	S	Q	I	T	P	H	A	I	I	F	L	P	N	T	D	G	M	E	M	L	1221
ZC4_h	DL	I	A	I	G	S	E	K	R	L	K	I	F	F	S	S	A	D	G	Y	H	L	I	D	A	E	S	E	V	M	S	D	V	T	L	P	K	N	P	L	E	I	I	I	P	Q	N	I	I	L	P	D	C	L	G	I	G	M	M	240

Fig. 3F

ZC504.4_ce
NIK_m
ZC1_h
ZC2_h
ZC3_h
ZC4_h

L	C	Y	D	N	E	G	V	Y	V	N	T	Y	G	R	M	T	K	N	V	V	L	Q	W	G	E	M	P	S	S	V	A	Y	I	S	T	G	Q	I	M	G	W	G	N	K	A	I	E	I	R	S	V	D	T	G	H	L	D	G	V
V	C	Y	E	D	E	G	V	Y	V	N	T	Y	G	R	I	T	K	D	V	V	L	Q	W	G	E	M	P	T	S	V	A	Y	I	R	S	N	Q	T	M	G	W	G	E	K	A	I	E	I	R	S	V	E	T	G	H	L	D	G	V
V	C	Y	E	D	E	G	V	Y	V	N	T	Y	G	R	I	T	K	D	V	V	L	Q	W	G	E	M	P	T	S	V	A	Y	I	R	S	N	Q	T	M	G	W	G	E	K	A	I	E	I	R	S	V	E	T	G	H	L	D	G	V
V	C	Y	E	D	E	G	V	Y	V	N	T	Y	G	R	I	T	K	D	V	V	L	Q	W	G	E	M	P	T	S	V	A	Y	I	H	S	N	Q	I	M	G	W	G	E	K	A	I	E	I	R	S	V	E	T	G	H	L	D	G	V
L	C	Y	E	D	E	G	V	Y	V	N	T	Y	G	R	I	T	K	D	V	V	L	Q	W	G	E	M	P	T	S	V	A	Y	I	C	S	N	Q	I	M	G	W	G	E	K	A	I	E	I	R	S	V	E	T	G	H	L	D	G	V
L	T	F	N	A	E	A	L	S	V	E	A	N	E	Q	L	F	K	K	I	L	E	M	W	K	D	I	P	S	S	I	A	F	E	C	T	D	R	T	T	G	W	G	Q	K	A	I	E	V	R	S	L	Q	S	R	V	L	E	S	E

ZC504.4_ce
NIK_m
ZC1_h
ZC2_h
ZC3_h
ZC4_h

F	M	H	K	K	A	Q	K	L	K	F	L	C	E	R	N	D	K	V	F	F	S	A	K	G	G	S	C	Q	I	Y	F	M	T	L	N	K	P	G	L	T	N	W					
F	M	H	K	R	A	Q	R	L	K	F	L	C	G	R	N	D	K	V	F	F	S	S	V	R	S	G	G	S	Q	V	Y	F	M	T	L	G	R	T	S	L	L	S	W				
F	M	H	K	R	A	Q	R	L	K	F	L	C	E	R	N	D	K	V	F	F	A	S	V	R	S	G	G	S	Q	V	Y	F	M	T	L	G	R	T	S	L	L	S	W				
F	M	H	K	R	A	Q	R	L	K	F	L	C	E	R	N	D	K	V	F	F	A	S	V	R	S	G	G	S	Q	V	F	F	M	T	L	N	R	N	S	M	M	N	W				
F	M	H	K	R	A	Q	R	L	K	F	L	C	E	R	N	D	K	V	F	F	A	S	V	R	S	G	G	S	Q	V	Y	F	M	T	L	N	R	I	M	N	W						
L	K	R	R	S	I	K	K	L	R	F	L	C	T	R	G	D	K	L	E	F	T	S	T	L	R	N	H	S	R	V	Y	F	M	T	L	G	K	L	E	E	L	Q	S	N	Y	D	V

Fig. 3G


```

* . . . * . . . *
KHS1_h 362 -SDPNFMLQWNP-----FV-----D 375
KHS2_h 359 LDSSEEIYYTARSNLDLQLEYGQGHGQGYFLGANKSLLKSVEEELHQRGHVAHLEDEGD 418

* . . . * . . . *
KHS1_h 376 GANTGKSTSKRAIPPLPKPRISSYPED-NFPDEEKASTIKHCP--DSESRAPIILRRQ 432
KHS2_h 419 DDESKHSTLKAKIPPLPKPKSIFIPQEMHSTEDENQGTIKRCPMMSGSPAKPSQVPPRP 478

* . . . * . . . *
KHS1_h 433 SSPSCGPVAETSSIGNGDGISKL-MSENTEGSA-----QAPQLPRKNDKRDFFPKPAIN 484
KHS2_h 479 PPPR--LPPHKPVALGNGMSSFQLMGERDGSQCQQQNEHRGTNLSRK-EKKDVPKPISN 534

* . . . * . . . *
KHS1_h 485 GLPPTPKVLMGACFSKVFDGCPKINCATSWIHPDTKDQYIIFGTEDGIYTLNLNELHEA 544
KHS2_h 535 GLPPTPKVHMGACFSKVFNCGCPKIHCASSWINPDTRDQYLIFGAEEGIYTLNLNELHET 594

* . . . * . . . *
KHS1_h 545 TMEQLFPRKCTWLVIINNLTMSLSEKTFQLYSHNLIALFEHAK-KPGLAAHIQTHRFPD 603
KHS2_h 595 SMEQLFPRRCTWLVIYMNCLLSIS-GKASQLYSHNLPGLFDYARQMQLPVAIPAHLPD 653

* . . . * . . . *
KHS1_h 604 RILPRKFALTITKIPDTKGCHKCCIVRNPNPYTGHKYLCGALQSGIVLLQWYEPMQKFMLIKH 663
KHS2_h 654 RILPRKFSVSAKIPETKWCQKCCVVRNPNPYTGHKYLCGALQTSIVLLEWVEPMQKFMLIKH 713

```

Fig. 4B

15/76

SULU_ce	L I Q R T K N M V L E L D N F Q Y K K M R K L L M Y L D E T E G K E G S E G N G A S D D L D F H G N E A N S I G R A G D S	360
SULU1_h	L I Q R T K D A V R E L D N L Q Y R K M K K I L F - - - - -	313
SULU3_m	L I Q R T K D A V R E L D N L Q Y R K M K K L L F - - - - -	309
SULU3_h	L I Q R T K D A V R E L D N L Q Y R K M K K L L F - - - - -	103

Fig. 5A

SULU_ce ASSRSASLT SFRSMQSSGGAGLLVSTNTTGAMDNVHSSGYGNGSSSTSSARRRRPPIPS 420
SULU1_h ----- QETRNGLNE S 324
SULU3_m ----- QEAHNGPAVEA 320
SULU3_h ----- QEAHNGPAVEA 114

SULU_ce QMLSSSTSTSGVG T M P S H G S V G A S I T A I A V N P T P S P S E P I P T S Q P T S K S E S S - S I L E T A H D 479
SULU1_h Q E D E E D S E H G T S L N R E M D S L G S N H S I P S M S V S T G S Q S S S V N S M Q E V M D E S S E L V M M H D D 384
SULU3_m Q E E E E E Q D H G V G R T G T V N S V G S N Q S I P S M S I S A S S Q S S S V N S L P D A S D D K S - E L D M M E G D 379
SULU3_h Q E E E E E Q D H G V G R T G T V N S V G S N Q S I P S M S I S A S S Q S S S V N S L P D V S D D K S - E L D M M E G D 173

SULU_ce D P L D T S I ----- R A P V K D L H M P H R A V K E R I A T L Q N H K F A T L R S Q R I I 521
SULU1_h E S T I N S S S S V V H K K D H V F T R D E A G H G D P R P E P R P T Q S V Q S Q A L H Y R N R E R F A T I K S A S L V 444
SULU3_m H T V M S N S S V I H L K P E E E N Y Q E E G D P R T R A S D P P Q S P P Q V S R H K S H Y R N R E H F A T I R T A S L V 439
SULU3_h H T V M S N S S V I H L K P E E E N Y R E E G D P R T R A S D P P Q S P P Q V S R H K S H Y R N R E H F A T I R T A S L V 233

SULU_ce N Q E Q E E Y T K E N N M Y E Q M S K Y K H L R Q A H H K E L Q Q F E R C A L D R E Q L R V K M D R E L E Q L T T T Y 581
SULU1_h T R Q I H E H E Q E N E L R E Q M S G Y K R M R R R Q H Q K Q L I A L E N K L K A E M D E H R L K L Q K E V E T H A N N S 504
SULU3_m T R Q M Q E H E Q D S E L R E Q M S G Y K R M R R R Q H Q K Q L M T L E N K L K A E M D E H R L R L D K D L E T Q R N N F 499
SULU3_h T R Q M Q E H E Q D S E L R E Q M S G Y K R M R R R Q H Q K Q L M T L E N K L K A E M D E H R L R L D K D L E T C R N N F 293

SULU_ce S K E K M R V R C S Q N N E L D K R K K D I E D G E K K M K K T K N S Q N Q Q Q M K L Y S A Q Q L K E Y K Y N K E A Q K 641
SULU1_h S I E L E K L A K K Q V A I I E K E A K V A A D E K K F Q Q Q I L A Q Q K K D L T T F L E S Q K K Q Y K I C K E K I K 564
SULU3_m A A E M E K L I K K H Q A A M E K E A K V M A N E E K K F Q Q H I I Q A Q Q K K E L N S F L E S Q K R E Y K L R K E Q L K 559
SULU3_h A A E M E K L I K K H Q A A M E K E A K V M S N E E K K F Q Q H I I Q A Q Q K K E L N S F L E S Q K R E Y K L R K E Q L K 353

Fig. 5B

SULU_ce TRLRSLNM-PRSTYENAMKEVKADLN RVKDAARENDFDEKLRRAELED EIVRYRQQQLSNLH 700
SULU1_h EEMNEDEHSTPKKEKQERISKHKENLQHTTQAEEEEAHLLTQQRLYYDKNCRFFKRRKIMIKRH 624
SULU3_m EELNENQSTPKKEKQEWLSKQKENIQHFQAEEEEANLLRRQRQYLELECCRFFKRRMLLGRH 619
SULU3_h EELNENQSTPKKEKQEWLSKQKENIQHFQAEEEEANLLRRQRQYLELECCRFFKRRMLLGRH 413

SULU_ce QLEEQQLDDEVDVNVQERQM DTRHGLLSKQHEMTRDLEIQHLNELHAMKKRHLETQHEAES 760
SULU1_h EVEQQNIREEELNKKRTQKEME HAMLIRHDESTRELEEYRQLHTLQKLRMDLIRLQHQTLE 684
SULU3_m NLEQDLVREEELNKKRQTQKDL EHAMLLRQHESMQELEEFRLHNTTIQKMRCELIRLQHQTLE 679
SULU3_h NLEQDLVREEELNKKRQTQKDL EHAMLLRQHESMQELEEFRLHNTTIQKMRCELIRLQHQTLE 473

SULU_ce SQNEYTYTQRQQDELRKKHAKMSRQQPRDLKIQEAQIRKQYRQVVKTQTRQFKLYLTQM VQV 820
SULU1_h NQLEYNKKRRERELHRKKHVMGLRQQPKNLKAMEMQIKKQFQDTCKVQTQKQYKALKNHQLE 744
SULU3_m NQLEYNKKRRERELRRKKHVM EVRQQPKSLKSKELQIKKQFQDTCKIQTROYKALRNHLL 739
SULU3_h NQLEYNKKRRERELRRKKHVM EVRQQPKSLKSKELQIKKQFQDTCKIQTROYKALRNHLL 533

SULU_ce VPKDEQKELTSRLKQDQM QKVALLASQYESQIKKMMVQDKTVKLESWQED EQRVLSEKLEK 880
SULU1_h TPKNNEHKTILKTLKDEQTRKLLAILAEQYEQSINEMMASQALRLDEAQEAECQALRLQLQ 804
SULU3_m TPKNNEHKA I 748
SULU3_h TPKSEHKA VLRKLKEEQTRKLLAILAEQYDHSINEMLS TQALRLDEAQEAECQV LKMQQLQ 593

SULU_ce ELEELIAYQKKTRATLEEEQIKKERTALEEIRIGTRRAMLEQKIIIEE REQMGE MRRLLKKEQI 940
SULU1_h EMELLNAYQSKIKMQTEAQHEREELQKLEQRVSLRRALHLEQKIEEEL AALQKER SERIKNL 864
SULU3_h ELEELLNAYQSKIKMQAE AQH DRELEQRVSLRRALLEQKIEEEL M LALQNER TERIRSL 653

Fig. 5C

SULU_ce RDRHSQERHRLLENHFVRRITGSTRSSGGIAPGVGNSSSIQMAM 982
SULU1_h LERQEREIETFDMESLRLMGFGNLTLDFFPKEDYR 898
SULU3_h LERQAREIEAFDSESMRLGFSNMVLSNLSPEAFSHSYPGASGWSHNPTGGPGPHWGHPMG 713
SULU3_h GPPQAWGHPMQGGPPQWGHPSGPMQGVPRGSSMGVRNSPQALRRRTASGGRTEQGMSRSTS 773
SULU3_h VTSQISNGSHMSYT 787

Fig. 5D

```

*****
1 MAFANFRRIILRLSTFEKRKSREYEHVRRDLDPNDVWEIVGELGDGAFGKVYKAKNKETGA 60
1 MAFANFRRIILRLSTFEKRKSREYEHVRRDLDPNEVWEIVGELGDGAFGKVYKAKNKETGA 60

*****
61 LAAAKVIETKSEEELEDYIVEIEILATCDHPYIVKLLGAYYYDGKLIWIMIEFCPGGAVDA 120
61 LAAAKVIETKSEEELEDYIVEIEILATCDHPYIVKLLGAYYHDGKLIWIMIEFCPGGAVDA 120

*****
121 IMLELDRGLTEPQIQVVCQMLEALNFLHGKRIIHRDLKAGNVLMTLEGDIRLADFGVSA 180
121 IMLELDRGLTEPQIQVVCQMLEALNFLHRSKRIIHRDLKAGNVLMTLEGDIRLADFGVSA 180

*****
181 KNLKTLQKRDSFIGTPYWMAPEVVLCEVTKMDAPYDYKADIWSLGITLIEMAQIEPPHHEL 240
181 KNLKTLQKRDSFIGTPYWMAPEVVMCEVTKMDTPYDYKADIWSLGITLIEMAQIEPPHHEL 240

*****
241 NPMRVLLKIAKSDPPTLLTPSKWSVEFRDFLKIALDKNPETRPSAAQLLQHPFVSRVTSN 300
241 NPMRVLLKIAKSDPPTLLTPSKWSVEFRDFLKIALDKNPETRPSAAQLLEHPFVSSITSN 300

*****
301 KALRELVAEAKAEVMEEIEDGREDEEEDAVDAVPLVNHTQDSANVTQPSLDSNKLQD 360
301 KALRELVAEAKAEVMEEIEDGREDEEEDAVDAASTLENHTQNSSEVSPPSLNADKPLEE 360

```

Fig. 6A

LOK_m 361 S-STPLPPSQPEPVNGPCSQPSGDGGLQTTSPADGLSKNDNDLKVPVPLRKSRPLSMDA 419
GEK2_h 361 SPSTPLAPSQSQDSVNEPCSQPSGDRSLQTTSPVAVPGNENGLAVPPLRKSRPVSM DA 420

LOK_m 420 RIQMDEEKQIPDQDENPSPAASKSQKANQSRPNSSALETLGGEALTNGGLELPSSVTPSH 479
GEK2_h 421 RIQVAQEKQVAEQGGDLSPAANRSQKASQSRPNSSALETLGGEKLANGSLEPPAQAAPGP 480

LOK_m 480 SKRASDCSNLSTSESM DYGTSLSADLSLNKETGSLSLKGSKLHNKTLKRTRRFVVDGVEV 539
GEK2_h 481 SKRDSDCSSLCTSESM DYGTNLSTDL SLNKEMGSLSIKDPKLYKTLKRTRKFVVDGVEV 540

LOK_m 540 SITTSKIISEDEKKDEEMRFLRRQELRELRL LQKEEHRNQTQLSSKHLEQLQM HKRFEQ 599
GEK2_h 541 SITTSKIISEDEKKDEEMRFLRRQELRELRL LQKEEHRNQTQLSNKHLEQLQM HKRFEQ 600

LOK_m 600 EINAKKKFYDVELENLERQQKQVEKMEQDHSVRRKEEAKRIRLEQDRDYAKFQEQLKQM 659
GEK2_h 601 EINAKKKFFDTELENLERQQKQVEKMEQDHAVRRREEARRIRLEQDRDYTRFQEQLKLM 660

LOK_m 660 KKEVKSEVEKLPQQRKESMKQKMEEHSQKKQRLDRDFVAKQKEDLELAMRKLTTENRRE 719
GEK2_h 661 KKEVKNEVEKLPQQRKESMKQKMEEHTQKKQLDRDFVAKQKEDLELAMKRLTTDNRRRE 720

```

*****
720 ICDKERDCLSKKQELLRDREAALWEMEEHQLQERHQLVKQQLKDQYFLQRHDLRLKHEKE 779
721 ICDKERECLMKKQELLRDREAALWEMEEHQLQERHQLVKQQLKDQYFLQRHELLRLKHEKE 780

*****
780 REQMQRYNQRMMEQLKVRQQQEKKARLPKIQRSDGETRMAMYKKSLHINGAGSASEQREKI 839
781 REQMQRYNQRMIEQLKVRQQQEKKARLPKIQRSEGKTRMAMYKKSLHINGGGSAEQREKI 840

*****
840 KQFSQQEKKRQKAERLQQQKKHEHQMRDMVAQCESNMSELQQQNEKCYLLVEHETQKCLK 899
841 KQFSQQEKKRQKSERLQQQKKHENQMRDMLAQCESNMSELQQQNEKCHLLVEHETQKCLK 900

*****
911 ALDESHNQSLKE
912 ALDESHNQNLKE

```

Fig. 6C

PAK1_h	MSNGLDIQDKPPAPPMRNTSTMIGAGSKDAGTL	NHGS	KPLPP	NPEEK	KKKDRFYRSIL	59
PAK65_h	MEETQQKSHLELSA	----	NHSL	KPLPS	VPEEK	KPRHKIIISIFS
PAK3_m	-MSDSL DNEEKPPAPPLR	----	MNSNNRDSSAL	NHSS	KPLPMA	PPEEK
						NKKARLSIFPG
						54
PAK1_h	PGDK	TNKKKEKERPEIS	LP	PSDFEHTI	HVGFD	AVTGEFTGM
						PEQWARLLQTSNITK
						LS
						115
PAK65_h	GTEK	GSKKKEKERPEIS	PP	PSDFEHTI	HVGFD	TVTGEFTGM
						PEQWARLLQTSNITKL

						96
PAK3_m	GGDK	TNKKKEKERPEIS	LP	PSDFEHTI	HVGFD	AVTGEFTGI
						PEQWARLLQTSNITKL

						110
PAK4_h	----	MFR	KKKKRPEISA	PQN	FQHRVHT	SFDPKEGKFVGL
						PPQWQNI
						LDLRRPK
						PPVDP
						56
PAK1_h	----	----	----	----	----	----
						115
PAK65_h	----	----	----	----	----	----
						96
PAK3_m	----	----	----	----	----	----
						110
PAK4_h	SRITRVQLQPMKTVVRGSAMPVDGYISGLLNDIQKLSV	ISSNTLRGRSPTSRRRAQSLGL	116			
PAK1_h	----	----	----	----	----	----
						115
PAK65_h	----	----	----	----	----	----
						96
PAK3_m	----	----	----	----	----	----
						110
PAK4_h	LGDEHWATDPDMYLQSPQSER	TDPHGLYLS	CNCGGTPAGHKQMPWP	EPQSPRVLP	PNGLAAK	176
PAK1_h	----	----	----	----	----	----
						127
PAK65_h	----	----	----	----	----	----
						108
PAK3_m	----	----	----	----	----	----
						122
PAK4_h	AQSLGPAEFQGASQRCLQLGAC	LQSSPPGAS	PPTGTNRHGMKA	AKHGS	EEAR	PQSC
						LVGS
						236

Fig. 7A

PAK1_h	L	E	F	Y	N	S	K	K	T	S	N	S	Q	K	Y	M	S	F	T	--	D	K	S	A	E	D	Y	N	S	S	N	A	L	N	V	K	A	V	S	E	T	P	A	V	P	P	V	S	E	D	E	D	D	D	D	D	A	T	185																		
PAK65_h	L	K	F	Y	D	S	--	N	T	V	K	Q	K	Y	L	S	F	T	--	P	P	E	K	D	G	F	P	S	G	T	P	A	L	N	A	K	G	T	E	A	P	A	V	T	--	E	E	E	D	D	D	E	E	T	160																						
PAK3_m	L	K	F	Y	D	S	K	E	T	V	N	N	Q	K	Y	M	S	F	T	S	G	D	K	S	A	H	G	Y	I	A	A	H	Q	S	N	T	K	T	G	S	E	P	L	A	P	P	V	S	E	E	E	E	E	E	E	E	182																				
PAK4_h	A	T	G	R	P	G	G	E	G	S	P	S	P	K	I	T	R	E	S	S	L	K	R	R	L	F	R	S	M	F	L	S	T	A	A	T	A	P	P	S	S	S	K	P	P	P	Q	S	K	P	N	S	S	F	R	P	P	Q	K	296																	
PAK5_h	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	A	S	G	A	K	L	A	A	G	R	P	F	N	T	14												
PAK1_h	--	--	--	--	P	P	P	V	I	A	P	R	P	E	H	T	K	S	V	Y	T	R	S	V	I	E	P	L	P	V	T	P	T	R	D	V	A	T	S	P	I	S	P	T	E	N	N	T	T	P	P	D	A	L	T	L	N	T	E	K	241																
PAK65_h	--	--	--	--	A	P	P	V	I	A	P	R	P	D	H	T	K	S	I	Y	T	R	S	V	I	D	P	V	P	A	P	V	G	D	S	H	V	D	G	A	A	K	S	L	--	--	--	--	--	--	--	--	--	--	--	--	--	D	K	202																	
PAK3_m	--	--	--	--	D	D	N	E	P	P	P	V	I	A	P	R	P	E	H	T	K	S	I	Y	T	R	S	V	E	S	I	A	S	P	A	A	P	N	K	E	D	I	P	P	S	A	E	N	A	N	S	T	T	L	Y	R	--	--	N	T	D	R	239														
PAK4_h	--	--	--	--	D	N	P	P	S	L	V	A	K	A	Q	S	L	P	S	D	Q	P	V	G	T	F	S	P	L	T	T	S	D	T	S	S	P	Q	K	S	L	R	T	A	P	A	T	G	Q	L	P	G	R	S	S	P	A	--	--	G	S	P	R	353													
PAK5_h	--	--	--	--	Y	P	R	A	D	T	D	H	P	S	R	G	A	Q	G	E	P	H	D	V	A	P	N	G	P	S	A	G	G	L	A	I	P	Q	S	S	S	S	S	S	R	P	P	T	R	A	R	G	A	P	S	P	G	V	L	G	P	H	A	S	74												
PAK1_h	Q	K	K	K	P	K	M	S	D	E	E	I	L	E	K	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	L	R	S	I	V	S	V	G	D	P	K	K	K	Y	T	R	F	E	K	I	276			
PAK65_h	Q	K	K	K	T	K	M	T	D	E	E	I	H	E	K	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	L	R	T	I	V	S	I	G	D	P	K	K	K	Y	T	R	Y	E	K	I	237	
PAK3_m	Q	R	K	K	S	K	M	T	D	E	E	I	L	E	K	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	--	L	R	S	I	V	S	V	G	D	P	K	K	K	Y	T	R	L	E	K	I	274
PAK4_h	T	W	H	A	Q	I	S	T	S	N	L	Y	L	P	Q	D	P	T	V	A	K	G	A	L	A	G	E	D	T	G	V	V	T	H	E	Q	F	K	A	A	L	R	M	V	V	D	Q	G	D	P	R	L	L	L	D	S	Y	V	K	I	413																
PAK5_h	E	P	Q	L	A	P	P	A	C	T	P	A	A	V	P	G	P	P	R	S	P	Q	R	E	P	Q	R	V	S	H	E	Q	F	R	A	A	L	Q	L	V	V	D	P	G	D	P	R	S	Y	L	D	N	F	I	K	I	134																				
PAK1_h	G	Q	G	A	S	G	T	V	Y	T	A	M	D	V	A	T	G	Q	E	V	A	I	K	Q	M	N	L	Q	Q	P	K	K	E	L	I	I	N	E	I	L	V	M	R	E	N	K	N	P	N	I	V	N	Y	L	D	S	Y	L	V	336																	
PAK65_h	G	Q	G	A	S	G	T	V	F	T	A	T	D	V	A	L	G	Q	E	V	A	I	K	Q	I	N	L	Q	Q	P	K	K	E	L	I	I	N	E	I	L	V	M	K	E	L	K	N	P	N	I	V	N	F	L	D	S	Y	L	V	297																	
PAK3_m	G	Q	G	A	S	G	T	V	Y	T	A	L	D	I	A	T	G	Q	E	V	A	I	K	Q	M	N	L	Q	Q	P	K	K	E	L	I	I	N	E	I	L	V	M	R	E	N	K	N	P	N	I	V	N	Y	L	D	S	Y	L	V	334																	
PAK4_h	G	E	G	S	T	G	I	V	C	L	A	R	E	K	H	S	G	R	Q	V	A	V	K	M	M	D	L	R	K	Q	Q	R	R	E	L	L	F	N	E	V	I	M	R	D	Y	Q	H	F	N	V	V	E	M	Y	K	S	Y	L	V	473																	
PAK5_h	G	E	G	S	T	G	I	V	C	I	A	T	V	R	S	S	G	K	L	V	A	V	K	M	D	L	R	K	Q	Q	R	R	E	L	L	F	N	E	V	I	M	R	D	Y	Q	H	E	N	V	V	E	M	Y	N	S	Y	L	V	194																		

Fig. 7B

PAK1_h	GDELWVVM EYLAGGSLTDVVVTETCMDEGQIAAVCRECLQAL	ESLH	SNQVIHRDIKSDN	IL	396					
PAK65_h	GDEL[FVVM EYLAGR]SLTDVVVTETCMDEAQIAAVCRECLQAL	EFLH	ANQVIHRDIKSDN	VL	357					
PAK3_m	GDELWVVM EYLAGGSLTDVVVTETCMDVGGQIAAVCRECLQAL	DFLH	SNQVIHRDIKSDN	IL	394					
PAK4_h	G[E]ELWV[L]M[E]F[L]QGGALTDI[VSQVRLN]EEQIA[TVCEAVL]QAL	AYLH	AQGV IHRDIKSD	SIL	533					
PAK5_h	GDELWVVM EYFLEGGALTDI[VTHT]RMNEEQIAAVCLAVLQAL	SVLH	AQGV IHRDIKSD	SIL	254					
PAK1_h	LGM DGSVKLTDFGFCAQITPEQSKRSTMVGTPYWM APEVVT	TRKAYGPKVDI	WSL	GIM AIE	456					
PAK65_h	LGM[E]GSVKLTDFGFCAQITPEQSKRSTMVGTPYWM APEVVT	TRKAYGPKVDI	WSL	GIM AIE	417					
PAK3_m	LGM DGSVKLTDFGFCAQITPEQSKRSTMVGTPYWM APEVVT	TRKAYGPKVDI	WSL	GIM AIE	454					
PAK4_h	L[TL]DGRVKLSDFGFCAQISKDVPKRKS[L]VGTPYWM APEV[ISRSL]YA	TEV	VDI	WSL	GIM VIE	593				
PAK5_h	L[THD]GRVKLSDFGFCAQVSK[E]VPRRKSLVGTPYWM APELIS	RPLPYGPIE	VDI	WSL	GIM VIE	314				
PAK1_h	MIEGEPYPYL NENPLRALYLIATNGTPELQNPEKLSAIFRD	FLNRCLEMDV	EKRGS	AKELL	516					
PAK65_h	MVEGEPYPYL NENPLRALYLIATNGTPELQNPEKLSPIIFRD	FLNRCLEMDV	EKRGS	AKELL	477					
PAK3_m	MVEGEPYPYL NENPLRALYLIATNGTPELQNPEL	SAV[FH]D	FLNRCLEMDV	DRRGS	AKELL	514				
PAK4_h	MVDGEPYPYFSDSPVQAMKRLRDSPPK[L]KN[SHK]VSPVLR	DRD	FLERM	LV	RD	QERAT	QELL	653		
PAK5_h	MVDGEPYPYFNEPPL[K]AMKM[I]RD[N]LPRLK[NL]HKVSP	SLK	GFL	DRLL	V	RD	PA	QRA	TAAELL	374
PAK1_h	QH[Q]FLK[I]AKPLSSLTPLIIAAAKEA	T	KNNH		545					
PAK65_h	QHPFLK[L]AKPLSSLTPLIIMAAAKEA	M	KSNR		506					
PAK3_m	QHPFLK[L]AKPLSSLTPLIIIAAKEA	I	KNSR		544					
PAK4_h	DHPFL[Q]TGLPEC[L]VPLI[Q]LYRKQTSTC				681					
PAK5_h	KHPFLAKA[G]PPA[S]IVPLMRQNRTR				398					

Fig. 7C

SEQ ID NO: 5 STLK2 human Nterm=1-21 kin=22-274
Cterm=275-416

MAHSPVAVQVPGMQNNIADPEELFTKLERIGKGSFGEVFKGIDNRTQQVVAIKIIDLEEA
EDEIEDIQEITVLSQCDSSYVTKYYSYLGSKLWIIMEYLGSGSALDLLRAGPFDEFQ
IATMLKEILKGLDYLHSEKKIHRDIKAANVLLSEQGDVKLADFGVAGQLTDTQIKRNTFV
GTPFWMAPEVIQQSAYDSKADIWSLGITAIELAKGEPPNSDMHPMRVLFLLIPKNNPPTLV
GDFTKSFKEFIDACLNKDPSFRPTAKELLKHKFIVKNSKTSYLTTELIDRFKRWKAEGHS
DDES DSEGS DSESTSRENTHPEWSFTTVRKKPDPKKVQNGAEQDLVQTLSCLSMIITPA
FAELKQQDENNASRNQAIEELEKSI AVAEAAACPGITDKMVKKLIEKFQKCSADESP

SEQ ID NO: 6 STLK3 human Nterm=1-31 kin=32-308 Cterm=309-489
(insert=327-352) tail=490-516

TAAPAPAAPAAPAPAPAPAPAAQAVGWPICRDAYELQEVIGSGATAVVQAALCKPRQERV
AIKRINLEKCQTSMDLLKEIQAMSQC SHPNVVTTYTSFVVKDELWLVMKLLSGGSMLDI
IKYIVNRGEHKNVLEEAIIATILKEVLEGLDYLRNGQIHRDLKAGNILLGEDGSVQIA
DFGVSAFLATGGDVTRNKVRKTFVGTPCWMAPEVMEQVRGYDFKADMWSFGITAIELATG
AAPHYHKYPPMKVLM LTLQNDPPTLETGVEDKEMMKKYGKSFRKLLSLCLQKDPSKRPTAA
ELLKCKFFQKAKNREY LIEKLLTRTPDIAQRAKKVRRVPGSSGHLHKTEDGDWEWSDDDEM
DEKSEEGKAAFSQEKSRRVKEENPEIAVSASTIPEQIQSLSVHDSQGPPNANEDYREASS
CAVNLVLRRLRNSRKELNDIRFEFTPGRDTADGVSQELFSAGLVDGHDVVIVAANLQKIVD
DPKALKTLTFKLASGCDGSEIPDEVKLIGFAQLSVS

SEQ ID NO: 7 STLK4 human Nterm=absent, kin=1-178, Ctail=179-414,
insert1=198-222, insert2=253-293

KSGVLDXSTIATILREVLEGLEYLHKXGQIHRDVKAGNILXGEDGSVQIADFGVSAFLAT
GGDITRNKVRKTFVGTPCWMAPEVMEQVRGYDFKADIWSFGITAIELATGAAPHYHKYPPM
KVLMLTLQNDPPSLETGVQDKEMKKYGKSFRKMISLCLQKDPEKRPTAAELLRHKFFQK
AKNKEFLQEKT LQ RAPTISERAKKVRVP GSSGRLHKTEDGGWEWSDDDEFDEESEEGKAA
ISQLRSPRVKESISNSELFP TTD PVGTL LQVPEQISAHLPQPAQGIATQPTQVSLPPTAE
PAKTAQALSSGSGSQETKIPISLVRLRNSKKELNDIRFEFTPGRDTAEGVSQELISAGL
VDGRDLVIVAANLQKIVEEPQSNRSVTFKLASGVEGSDIPDDGKLIGFAQLSIS

SEQ ID NO: 8 STLK5 human Nterm=absent, kin=1-222(lacks N-term),
Ctail=224-274

LICTHFMDGMNELAIAYILQGV LKALDYIHHMGYVHRSVKASHILISVDGKVYLSGLRSN
LSMISHGQRQRVVHDFPKYSVKVLPWLSPEVLQQNLQGYDAKSDIYSVGITACELANGHV
PFKDMPATQMLLEKLN GTVPCLLD TSTIPAEELTMSPSRSVANSGLSDSLTTSTPRPSNG
DSPSHPHYHRTFSPHFHHFVEQCLQRNP DARPSASTLLNHSFFKQIKRRASEALPELLRPV

TPITNFEGSQSDHSGIFGLVTNLEELEVDWDF

SEQ ID NO: 13 ZC1 human 1/5/98 Nterm=1-22 kin=23-289

coiled-coil=290-526 pro=527-640 B=641-896 Rab/Rac-BD=897-1239

MANDSPAKSLVDIDLSSLRDPAGIFELVEVVGNGTYGQVYKGRHVKTGQLAAIKVMDVTE
DEEEEIKLEINMLKKYSHHRNIATYYGAFIKKSPPGHDDQLWLVMFECGAGSITDLVKNT
KGNTLKEDWIAYISREILRGLAHLHIHHVIHRDIKGQNVLLTENAEVKLVDFGVSAQLDR
TVGRRNTFIGTPYWMAPEVIACDENPDATYDYRSDLWSCGITAIEMAEGAPPLCDMHPMR
ALFLIPRNPPRLKSKKWSKKFFSFIEGCLVKNYMQRPSTEQLLKHPFIRDQPNERQVRI
QLKDHIDRTRKKRGEKDETEYEYSGSEEEEEVPEQEGEPSSIVNVPGESTLRRDFLRLO
QENKERSEALRRQQLLEQQQLREQEEYKRQLLAERQKRIEQQKEQRRRLEEQQRREREAR
RQQEREQRRREQEKKRRLEELERRRKEEEEERRRAEEEKRRVEREQEYIRRQLEEEQRHLE
VLQQQLLEQAMLLPCRWREMEHRQAERLQRQLQQEQAYLLSLQHDHRRPHPQHSQQPP
PPQQERSKPSFHAPEPKAHYEPADRAREVEDRFRKTNHSSPEAQSKQTGRVLEPPVPSRS
ESFSNGNSESVHPALQRPAPQVPVRTTSRSPVLSRRDSPLOQSGGQQNSQAGQRNSTSIE
PRLLWERVEKLVPRPGSGSSSGSSNSGSQPGSHPGSQSGSGERFRVRSSSKSEGSPSQR
ENAVKKPEDKKEVFRPLKPADLTALAKELRAVEDVRPPHKVTDYSSSSEESGTTDEEDDD
VEQEGADESTSGPEDTRAASSLNLSNGETESVKTMIVHDDVESEPAMTPSKEGTLIVRRT
QSASSTLQKHKSSSSFTPFIDPRLLQISPSSGTTVTSVVGFSFGDGMPEAIRQDPTRKGS
VVNVNPTNTRPQSDTPEIRKYKKRFNSEILCAALWGVNLLVGTESGLMLLDRSGQGKVYP
LINRRRFQQMDVLEGLNVLVLTISGKKDKLRVYYLSWLRNKLHNDPEVEKKQGWTTVGD
EGCVHYKVVKYERIKFLVIALKSSVEVYAWAPKPYHKFMAFKSFGELVHKPLLVDLTVEE
GQRLKVIYIGSCAGFHAVDVGSGSVYDIYLPHTHIQCSIKPHAIILPNTDGMELLVCYED
GVYVNTYGRITKDVVLQWGEMPTSVAYIRSNQTMGWGEKAIEIRSVETGHLDGVMHKRA
QRLKFLCERNKVFVFAVRSVSGSSQVYFMTLGRTSLLSW

SEQ ID NO: 14 ZC2 human Nterm=missing kin=1-255 coiled-coil=256-442
pro=443-626 B=627-954 Rab/RacBD=955-1297

AFGEVYEGRHVKTGQLAAIKVMDVTGDEEEEIKQEIINMLKKYSHHRNIATYYGAFIKKNP
PGMDDQLWLVMFECGAGSVTDLIKNTKGNTLKEEWIAYICREILRGLSHLHQHKVIHRDI
KGQNVLLTENAEVKLVDFGVSAQLDRTVGRRNTFIGTPYWMAPEVIACDENPDATYDFKS
DLWSLGITAIEMAEGAPPLCDMHPMRALFLIPRNPPRLKSKKWSKKFQSFIESCLVKNH
SQRPAEQLMKHPFIRDQPNERQVRIQLKDHIDRTRKKRGEKDETEYEYSGSEEEEEEND
SGEPSSILNLPRESTLRRDFLRQLANKERSEALRRQQLLEQQQRENEEHKRQLLAERQKR
IEEQKEQRRRLEEQQRRREKELRKQQEREQRRHYEEQMRREEERRRAEHEQEYKRKQLEEQ
RQAERLQRQLKQERDYLVSQHQHQEQRPVEKKPLYHYKEGMSPSEKPAWAKEVEEERSRL
NRQSSPAMPHKVANRISDPNLPRESSESFISGVQPARTPPMLRPVDPQIPHLVAVKSQGP
ALTASQSVHEQPTKGLSGFQEALNVTSHRVEMPRQNSDPTSENPLPTRIEKFDRSSWLR

Fig. 8B

27/76

QEEDIPPKVPQRTTSSISPALARKNSPGNGSALGPRLGSQPIRASNPDLRRTEPILESPLQ
RTSSGSSSSSSSTPSSQPSQGGSQPGSQAGSSERTRVRANSKSEGSVLPHEPAKVKEE
SRDITRPSRPASYKKAIDEDLTALAKELRELRIEETNRPMKKVTDYSSSSSEESSESEEE
EDGESETHDGTVAVSDIPRLIPTGAPGSNEQYNVGMVGTHGLETSHADSFSGSISREGTL
MIRETSGEKKRSGHSDSNGFAGHINLPDLVQQSHSPAGTPT EGLGRVSTHSQEMDSGTEY
GMGSSTKASFTPFVDPRVYQTSPTDEDEDEEESAAALFTGELLRQEQA KLN EARKISVV
NVNPTNIRPHSDTPEIRKYKKRFNSEILCAALWGVNLLVGTENGLMLLDRSGQGKVYNLI
NRRRFQQMDVLEGLNVLTISGKKNKLRVYYLSWLRNRILHNDPEVEKKQGWITVGDLEG
CIHYKVVKYERIKFLVIALKNAVEIYAWAPKPYHKFMAFKSFADLQHKPLLVDLTVEEGQ
RLKVIFGSHTGFHVIDVDSGNSYDIYTPSHIQGNITPHAIVILPKTDGMEMLVCYEDEGV
YVNTYGRITKDVVLQWGEMPTSVAYIHSNQIMGWGEKAIEIRSVETGHL DGVFMHKRAQR
LKFLCERN DKVFFASVRS GGSSQVFFMTLNRNSMMNW

SEQ ID NO: 15 ZC3 human kin=1-255 coiled-coil=256-476 pro=477-680
B=681-983 Rab/RacBD =984-1326

AFGEVYEGRHVKTGQLAAIKVMDVTEDEEEEIKQEINMLKKYSHHRNIATYYGAFIKKSP
PGNDDQLWLVMFCGAGSVTDLVKNTKGNALKEDCIAYICREILRGLAHLHAHKVIHRDI
KGQNVLLTENA EVKLVD FGVSAQLDRTVGRRNTFIGTPYWMAPEVIACDENPDATYDYRS
DIWSLGITAIEMAEGAPPLCDMHPMRALFLIPRNPPRLKSKKWSKKFIDFIDTCLIKTY
LSRPPT EQLLKFPFIRDQPTERQVRIQLKDHIDRSRKKRGEKEETEY EYSGSEEEDDSHG
EEGEPSSIMNVPGESTLRREFLRLQQENKSNSEALKQQQQQLQQQQQRDPEAHIKHLLHQR
QRRIEEQKEERRRVEEQRRREREQRKLQEKEQQRRLED MQALRREEERRQAEREQEYIRH
RLEEEQRQLEILQQQLLQE QALLLEYKRKQLEEQRQSERLQRQLQQEHAYLKS LQQQQQ
QQLQKQQQQQLLPGDRKPLYHYGRGMNPADKPAWAREVEERTRMNKQQNSPLAKSKPGST
GPEPPIPQASPGPPGPLSQTTPMQRVPEQEGPHKSLVAHRVPLKPYAAPVPRSQSLQDQ
PTRNLAAFPASHDPDPAIPAPTATPSARGAVIRQNSDPTSEGPGPSNPPAWVRPDNEAP
PKVPQRTSS IATA LNTSGAGGSRPAQAVRARPRSNSAWQIYLQRR AERGTPKPPGPPAQP
PGPPNASSNPDLRRSDPGWERSDSVLPASHGHL PQAGSLERNRVGVSSKPDSSPVLSPGN
KAKPDDHRSRPGRPADFVLLKERTLDEAPRPPKKAMDYSSSSSEEVESSEDEEEEGEGGPA
EGSRDTPGGRDGD TDSVSTMVVHDVEEITGTQPPYGGGT MVVQRTPEEERNLLHADSNGY
TNLPDVVQPSHSPTENSKGQSPPSKDGSGDYQSRGLVKAPGKSSFTMFVDLGIYQPGGSG
DSIPITALVGGEGTRLDQLQYDVRKGSVVNVNPTNTRAHSETPEIRKYKKRFNSEILCAA
LWGVNLLVGTENGLMLLDRSGQGKVYGLIGRRRFQQMDVLEGLNLLITISGKR NKLRVYY
LSWLRNKILHNDPEVEKKQGWTTVGDMEGCGHYRVVKYERIKFLVIALKSSVEVYAWAPK
PYHKFMAFKSFADLPHRPLLVDLTVEEGQRLKVIYGSSAGFHAVD VDSGNSYDIYIPVHI
QSQITPHAIIFLPNTDGMEMLLCYEDEGVYVNTYGR IIKDVVLQWGEMPTSVAYICSNQI
MGWGEKAIEIRSVETGHL DGVFMHKRAQR LKFLCERN DKVFFASVRS GGSSQVYFMTLNR
NRIMNW

Fig. 8C
28/76

SEQ ID NO: 16 ZC4 human Nterm kin coiled-coil pro B=missing
Rab/RacBD=1-349

NVNPLYVSPACKKPLIHMYEKEFTSEICCGSLWGVNLLLGTRSNLYLMDRSGKADITKLI
RRRPFRQIQVLEPLNLLITISGHKNRLRVYHLTWLRNKILNNDPESKRRQEEMLKTEEAC
KAIDKLTGCEHFSVLQHEETTYIAIALKSSIHLYAWAPKSFDESTAIKVFPPTLDHKPVTV
DLAIGSEKRLKIFFSSADGYHLIDAESEVMSDVTLPKNPLEIIIPQNIIILPDCLGIGMM
LTFNAEALSVEANEQLFKKILEMWKDIPSSIAFECTQRTTGWGQKAIEVRSLQSRVLESE
LKRRSIKKLRFLCTRGDKLFFTSTLRNHHSRVYFMTLGKLEELQSNDY

SEQ ID NO: 18 KHS2 human Nterm=1-13 kin=14-273 A=274-346
Pro=347-534 RabBD =535-894

MNPGFDLSRRNPQEDFELIQRIGSGTYGDVYKARNVNTGELAAIKVIKLEPGEDFAVVQQ
EIIMMKDCKHPNIVAYFGSYLRRDKLWICMEFCGGGSLQDIYHVTGPLSELQIAYVSRET
LQGLYYLHSGKGMHRDIKGANILLTDNGHVKLADFGVSAQITATIAKRKSFITPYWMA
EVAVERKGGYNQLCDLWAVGITAIELAEQPPMFDLHPMRALFLMTKSNFQPPKLKDKM
KWSNSFHHFVKMALTKNPKKRPTAEKLLQHPFVTQHLTRSLAIELLDKVNPNPDHSTYHDF
DDDDPEPLVAVPHRIHSTSRNVREEKTRSEITFGQVKFDPPLRKETEPHHELPDSDGFLD
SSEIIYYTARSNLDLQLEYGQGHQGGYFLGANKSLLKSVEEELHQRGHVAHLEDDEGDD
ESKHSTLKAKIPPLPPPKPSIFIPQEMHSTEDENQGTIKRCMSGSPAKPSQVPPRPPP
PRLPPHKPVALGNGMSSFQLNGERDGSQCQQQNEHRGTNLSRKEKKDVPKPI SNGLPPTP
KVHMGACFSKVFNGCPLKIHCASSWINPDTRDQYLIFGAEEGIYTLNLNELHETSMEQLF
PRRCTWLYVMNNCLLSISGKASQLYSHNLPGLFDYARQMQLPVAIPAHKLPDRILPRKF
SVSAKIPETKWCQKCCVVRNPYTGHKYL CGALQTSIVLLEWVEPMQKFMLIKHIDFPIPC
PLRMFEMLVVPEQEYPLVCVGVSRGRDFNQVVRFETVNPNSTSSWFTESDTPQTNVTHVT
QLERDTILVCLDCCIKIVNLQGRKSSRKLSSSELTDFDQIESIVCLQDSVLAFWKHGMQG
RSFRSNEVTQEISDSTRIFRLLGSDRVVLESRPTDNPTANSNLYILAGHENSY

SEQ ID NO: 22 SULU1 human N=1-21 kin=22-277 A=278-427
coiled-coil1=428-637 B=638-751 coiled-coil2=752-898

MRKGVLDKPEIDDLFYKDDPEELFIGLHEIGHGSFGAVYFATNAHTNEVVAIKKMSYSGK
QTHEKWQDILKEVKFLRQLKHPNTIEYKGCYLKEHTAWLVMYCLGSASDLLLVHKKPLQ
EVEIAAITHGALHGLAYLHSHALHRDIKAGNILLTEPGQVKLADFGSASMASPANSFVG
TPYWMAPEVILAMDEGQYDGKVDIWSLGITCIELAERKPPLFNMNAMSALYHIAQNDSP
LQSNEWTDSFRRFVDYCLQKIPQERPTSAELLRHDFVRRDRPLRVLIQRTKDAVREL
DNLQYRKMKKILFQETRNGPLNESQEDEEDSEHGTSLNREMSLGSNHSIPSM SVSTGSQ
SSSVNSMQEVMDSSSELVMMHDESTINSSSVVHKKDHVFTRDEAGHGDP RPEPRPTQ
SVQSQUALHYRNRERFATIKSASLVTRQIHEHEQENELREQMSGYKRMRRQHQQQLIALEN
KLKAEMDEHRLKLQKEVETHANNSSIELEKLAKKQVAIIEKEAKVAAADEKKFQQQILAQ

Fig. 8D

QKKDLTTFLESQKKQYKICKEKIKEEMNEDHSTPKKEKQERISKHKENLQHTQAEAAAHL
LTQQRLYYDKNCRFFKRKIMIKRHEVEQQNIREELNKKRTQKEMEAMHLIRHDESTRELE
YRQLHTLQKLRLDLIRLQHQTLENQLEYNKRERELHRKHVMGLRQQPKNLKAMEMQIK
KQFQDTCKVQTKQYKALKNHQLEVTTPKNEHKTILKTLKDEQTRKLAILAEQYEQSINEMM
ASQALRLDEAQEAECQALRLQLQQEMELLNAYQSKIKMQTEAQHERELQKLEQRVSLRRA
HLEQKIEEELAALQKERSERIKNLLERQEREIETFDMESLRMGFGNLVTLDFPKEDYR

SEQ ID NO: 23 SULU3 human Nterm=missing kin partial=1-66 A=67-215
coiled-coil1=216-425 B=426-539 coiled-coil2=540-786 Ctail=687-786
IELAERKPPLFNMNAMSALYHIAQNESPTLQSNEWSDYFRNFVDSCLQKIPQDRPTSEEL
LKHIFVLRRERPETVLIDLIQRTKDAVRELDNLQYRKMKLLFQEAHNGPAVEAQEEEEEQ
DHGVGRTGTVNSVGSNQSIPTSMSSISASSQSSSVNSLPDVSDDKSELDMMEGDHTVMSNSS
VIHLKPEEENYREEGDPRTASDPQSPQVSRHKSHYRNREHFATIRTSASLVTRQMQEHE
QDSELREQMSGYKRMRRQHQQKQMTLENKLKAEMDEHRLRLDKDLETQRNNFAAEMEKL
KKHQAAMEKEAKVMSNEEKKFQQHIQAQQKKELNSFLESQKREYKLRKEQLKEELNENQS
TPKKEKQEWLSKQKENIQHFQAEAAEANLLRRRQRYLELECRFRKRRMLLGRHNLEQDLVR
EELNKRQTQKDLEHAMLLRQHESMQELEFRHLNTIQKMRCELIRLQHQTENQLEYNKR
RERELRRKHVMEVRQQPKSLKSKELQIKKQFQDTCKIQTRQYKALRNHLLLETPKSEHKA
VLKRLKEEQTRKLAILAEQYDHSINEMLSTQALRLDEAQEAECQVLKMQQLQEELELLNAY
QSKIKMQAEAQHDRELRELEQRVSLRRALLEQKIEEEMLALQNERTERIRSLERQAREI
EAFDSESMRLGFSNMVLSNLSPEAFSHSYPGASGWSHNPTGGPGPHWGHPMGPPQAWGH
PMQGGPQPWGHPSGPMQGVPRGSSMGVRNSPQALRRRTASGGRTAQGMSRSTSVTSQISNG
SHMSYT

SEQ ID NO: 24 SULU3 murine Nterm=1-25 kin=26-273 A=274-422
cc1=423-632 B=633-748 cc2=missing
MPSTNRAGSLKDPEIAELFFKEDPEKLFTDLREIGHGSFGAVYFARDVRTNEVVAIKKMS
YSGKQSTEKWQDIIKEVKFLQRIKHPSNIEYKGCYLREHTAWLVMYCLGSASDLLLEVHK
KPLQEEVEIAAITHGALQGLAYLHSHTMIHRDIKAGNILLTEPGQVKLADFGSASMASPAN
SFVGTPYWMAPEVILAMDEGQYDGKVDVWSLGITCIELAERKPPLFNMNAMSALYHIAQN
ESPTLQSNMNDSCCLQKIPQDRPTSEELLKHMFLRRERPETVLIDLIQRTKDAVRELDNLQ
YRKMKLLFQEAHNGPAVEAQEEEEEQDHGVGRTGTVNSVGSNQSIPTSMSSISASSQSSSV
NSLPDASDDKSELDMMEGDHTVMSNSSVIHLKPEEENYQEEGDPRTASDPQSPQVSRH
KSHYRNREHFATIRTSASLVTRQMQEHEQDSELREQMSGYKRMRRQHQQKQMTLENKLKAE
MDEHRLRLDKDLETQRNNFAAEMEKLKKHQAAMEKEAKVMAEKKFQQHIQAQQKKEL
NSFLESQKREYKLRKEQLKEELNENQSTPKKEKQEWLSKQKENIQHFQAEAAEANLLRRRQ
QYLELECRFRKRRMLLGRHNLEQDLVREELNKRQTQKDLEHAMLLRQHESMQELEFRHLN
TIQKMRCELIRLQHQTENQLEYNKRERELRRKHVMEVRQQPKSLKSKELQIKKQFQD

Fig. 8E
30/76

TCKIQTRQYKALRNHLLLETPKNEHKAI

SEQ ID NO: 26 GEK2 human N=1-33 kin=34-294 A=295-337 B=338-472 215
coiled-coil1=473-724 215 coiled-coil2=725-912

MAFANFRRLRLSTFEKRKSREYEHVRRDLDPNEVWEIVGELGDGAFGKVYKAKNKETGA
LAAAKVIETKSEEELEDYIVEIEILATCDHPYIVKLLGAYYHDGKLWIMIEFCPPGGAVDA
IMLELDRGLTEPQIQVVCQMLEALNFLHSKRRIHRDLKAGNVLMTLEGDIRLADFGVSA
KNLCTLQKRDSFIGTPYWMAPEVVMCETMKDTPYDYKADIWSLGITLIEMAQIEPPHHEL
NPMRVLLKIAKSDPPTLLTPSKWSVEFRDFLKIALDKNPETRPSAAQLLEHPFVSSITSN
KALRELVAEAKAEVMEEIEDGRDEGEEEDAVIDAASSTLENHTQNSSEVSPPSLNADKPLEE
SPSTPLAPSQSQDSVNEPCSQPSGDRSLQTTSPPVVAPGNENGLAVPVPLRKSRPVSMDA
RIQVAQEKQVAEQGGDLSPAANRSQKASQSRPNSSALETLGGEKLANGSLEPPAQAAPGP
SKRSDSCSSLCTSESMDYGTNLSTDLSLNKEMGSLSIKDPKLYKKTLLKRTKRFVVDGVEV
SITTSKIISEDEKKDEEMRFLRRQELRELRLQLKEEHRNQTQLSNKHELQLEQMHRFEQ
EINAKKKFFDTELENLERQQKQQVEKMEQDHAVRRREEARRIRLEQDRDYTRFQEQLKLM
KKEVKNEVEKLPRQQRKESMKQKMEEHTQKKQLLDRDFVAKQKEDLELAMKRLTTDNRR
ICDKERECLMKKQELLRDREAALWEMEEHQLQERHQLVKQQLKDQYFLQRHELLRKHEKE
REQMQRYNQRMIEQLKVRQQQEKARLPKIQRSEGKTRMAMYKKSLHINGGGSAAEQREKI
KQFSQQEEKRQKSERLQQQQKHENQMRDMLAQCESNMSELQQQLQNEKCHLLVEHETQKLK
ALDESHNQNKE

SEQ ID NO: 29 PAK4 human Rac=1-51 A=52-224 Nterm=225-393
kin=394-658 Ctail=659-681 residues 13-23

(SAPQNFQHRVH)= Cdc42 /Rac-binding motif

MFRKKKKKRPEISAPQNFQHRVHTSFDPKEGKFVGLPPQWQNILDTLRRPKPVVDPSRIT
RVQLQPMKTVVRGSAMPVDGYISGLLNDIQKLSVISSNTLRGRSPTSRRRAQSLGLLGDE
HWATDPDMYLQSPQSERTDPHGLYLSCNGGTPAGHKQMPWPEPQSPRVLPNGLAACAQSL
GPAEFQGASQRCLQLGACLQSSPPGASPTGTNRHGMKAACHGSEEARPQSCLVGSATGR
PGGEGSPSPKTRESSLKRRFLFRSMFLSTAATAPPSSSKPGPPPQSKPNSSFRPPQKDNPP
SLVAKAQSLLPSDQPVGTFSPLTTSDTSSPQKSLRTAPATGQLPGRSSPAGSPRTWHAQIS
TSNLYLPQDPTVAKGALAGEDTGVTHEQFKAALRMVVDQGDPRLLLLDSYVKIGEGSTGI
VCLAREKHSGRQVAVKMDLRKQQRRELLFNEVVIMRDYQHFNVEMYKSYLVGEELWVL
MEFLQGGALTDIVSQVRLNEEQIATVCEAVLQALAYLHAQGVHRDIKSDSILLTLDGRV
KLSDFGFCAQISKDVPKRKSLVGTPYWMAPEVISRSLYATEVDIWSLGIMVIEMVDGEP
YFSDSPVQAMKRLRDSPPPKLKNSHKVSPVLRDFLERMLVRDPQERATAQELLDPFLQ
TGLPECLVPLIQLYRKQTSTC

SEQ ID NO: 30 PAK5 human Rac A=missing Nterm partial=1-114
kin=115-379 Ctail=380-398

ASGAKLAAGRPFNTYPRADTDHPSRGAQGEPHDVAPNGPSAGGLAIPQSSSSSSSRPPTRA
RGAPSPGVLGPHASEPQLAPPACTPAAPAVPGPPGPRSPQREPQRVSHEQFRAALQLVVD
PGDPRSYLDFIKIGEGSTGIVCIATVRSSGKLVAVKKMDLRKQQRRELLFNEVVIMRDY
QHENVVEMYNSYLVGDELWVMEFLEGGALTDIVTHTRMNEEQIAAVCLAVLQALSVLHA
QGVHRDIKSDSILLTHDGRVKLSDFGFCAQVSKEVPRRKSLVGTPYWMAPELISRLPYG
PEVDIWSLGIMVIEMVDGEPPYFNEPPLKAMKMIRDNLPPRLKNLHKVSPSLKGFLDRLL
VRDPAQRATAAELLKHPFLAKAGPPASIVPLMRQNRTR

Fig. 8G

SEQ ID NO: 1 STLK2 HUMAN

TAACAGCCCACCTCCTAGCCCCGGGCTACGCGCCGCCAGCCCAGTAACCCCACTTTTGTG
TGTCCTCCCAGGCCCCGATCGAAAAGCCTGGGAGGGCCGCCGAACCTACCCCGGAGGGAG
GAGCCAGTCCGAACCCAAGGCGCCACCGCCGCAGAAGCGGAGCGAGGCAGCATTTCGCCTC
CATGGCCCCACTCGCCGGTGGCTGTCCAAGTGCCTGGGATGCAGAATAACATAGCTGATCC
AGAAGAAGTGTTCACAAAATTAGAGCGCATTGGGAAAAGGCTCATTTGGGGAAAGTTTTCAA
AGGAATTGATAACCGTACCCAGCAAGTCGTTGCTATTTAAAATCATAGACCTTGAGGAAGC
CGAAGATGAAATAGAAGACATTCAGCAAGAAATAACTGTCTTGAGTCAATGTGACAGCTC
ATATGTAACAAAATACTATGGGTCATATTTAAAGGGGTCTAAATTATGGATAATAATGGA
ATACCTGGGCGGTGGTTCAGCACTGGATCTTCTTCGAGCTGGTCCATTTGATGAGTTCCA
GATTGCTACCATGCTAAAGGAAATTTTAAAAGGTCTGGACTATCTGCATTTCAGAAAAGAA
AATTCACCGAGACATAAAAGCTGCCAATGTCTTGCTCTCAGAACAAGGAGATGTTAAACT
TGCTGATTTTGGAGTTGCTGGTCAGCTGACAGATACACAGATTAAAAGAAATACCTTTGT
GGGAACTCCATTTTGGATGGCTCCTGAAGTTATTCAACAGTCAGCTTATGACTCAAAAGC
TGACATTTGGTCATTGGGAATTACTGCTATTGAACTAGCCAAGGGAGAGCCACCTAACTC
CGATATGCATCCAATGAGAGTTCTGTTTCTTATTCCCAAAAACAATCCTCCAACCTCTTGT
TGGAGACTTTACTAAGTCTTTTAAGGAGTTTATTGATGCTTGCCTGAACAAAGATCCATC
ATTTTCGTCCTACAGCAAAAGAACTTCTGAAACACAAATTCATTGTAAAAAATTCAAAGAA
GACTTCTTATCTGACTGAACTGATAGATCGTTTTTAAGAGATGGAAGGCAGAAGGACACAG
TGATGATGAATCTGATTCCGAGGGCTCTGATTGGAATCTACCAGCAGGGAAAACAATAC
TCATCCTGAATGGAGCTTTACCACCGTACGAAAGAAGCCTGATCCAAAGAAAGTACAGAA
TGGGGCAGAGCAAGATCTTGTGCAAACCTGAGTTGTTTGTCTATGATAATCACACCTGC
ATTTGCTGAACTTAAACAGCAGGACGAGAATAACGCTAGCAGGAATCAGGCGATTGAAGA
ACTCGAGAAAAGTATTGCTGTGGCTGAAGCCGCCTGTCCCGGCATCACAGATAAAATGGT
GAAGAACTAATTGAAAAATTTCAAAGTGTTTCAGCAGACGAATCCCCCTAAGAACTTA
TTATTGGCTTCTGTTTTCATATGGACCCAGAGAGCCCCACCAAACCTACGTCAAGATTAAC
AATGCTTAACCCATGAGCTCCATGTGCCTTTTGGATCTTTGCAACACTGAAGATTTGGAA
GAAGCTATTAACTATTTTGTGATGGCGTTTATCATTTTATATTTTGAAGGATTATTTT
GTAAGGAATAACTTTTAATACTATAGTTTCACCTGTATTCTAGTAAATGTTGAGACACCG
TTTTGCTTTTAAGTATCCCTATTTCTTAAGTTACGAGGATGAATACCTTTTACATTTTGA
TCTTTAGTTGACTCTACAGTCATGAAACATACAGGTCTTTCAAAGTCATTCTCAATATTC
AGCTTTTGTAAATTATCAAGCTTCAAAAAGCTTTTTTTTTAAAAAACAACATGCATATT
CTAAAAATGACTATTGGTGGGGAGGTGTAAATAAGTCATACCTTCTTAAAACAGAAAATT
TAAGTAAAGTCTTTTAAATGAAACCTGTAAAAGTATTGACTCTTCTACCAAGTTGGTATG
ATATTCCAGGCAGCTCAATGATTATCACATTTGAGACCCTGTGTTTGAAGCATTTACAGG
CAATGTACAGCAACAGAGGTACCTCTTGGTGTATAGTATTTACATTCTCTTTTAGGTAGA
AGAGGCAATTTTACCCTTATTTACATGGTTAGAAATTTAAAGCAAGATCATTTACCCAA

Fig. 9A

GGATAGGTGTTTGGTAATGTTGAAGGAGTTAGTCTGGCTTCATGTTTTACATCTTCAACT
AAAATCCCATACTATCTGCTTGGATTTGGAGAGCCAAAAAATAAAGCTGATTGTCATGTG
ATTAAATATCTGATCAACAGGTATGAATATAACTTAAATCAGCATATTTTTGCCATGGTA
ATAAATTGTCCTATAAACTATTTATATATTTTTGTTCTTCATAATTATCACTAATAAGCA
TCAGTTTGTGTTTTTAAAAGGATATTTAAGTGAGCATTTTCTAGTTCATATGAAAATAA
CCATAGTACAGGATGATTTCTGTCCACACAAAGGTTAAATTAGATTGCACAGTTAATTTT
CACTTATATTTATGGTACTATTATGTGGGTGATGCCTTTTTTCTTTTAAGCCCAGTACATA
TATTATGCCTGCCTAAGTTCTGAACTGGGGCTGTATTTTCAGTAGTTGTAGAATTATTGAT
ATTTAGTTTTTGATAGCTAATGTTTAATTGTTTGGATCTGCACAGTTTGGTTTTTGCACAA
AAGTCATTTAAAAAAATCTGAGTAATTGTCAAATATTTAAAAGAAAGATATTCTTCCTGTA
AGGAATACAGTTTTTAGTCAAAGTGCCATTACATCCTCTTTTAAATTTACATAATACAG
ATACTTGAGAAAGTTGTTGTGGTGTGTATGCCAAGAAAATTCTTTTTATTGGTGCCTAT
ATTGTAACAATTATTTTTAATGCATTGTATTTTGAAGTAACGGTTCAGTTAAATTTTTCA
CCTGCTGTGTAAC TGAAACACAATTACAGTTTATAATCATCTGTAGAAGTCTGGAGATAA
TTTTGCAACTCATGTTATGGGTAAATGAATATTTTTGTAAAAGTAAAAGCAACAAATTT
ATAAATTGATTATTTGAAACTTTACAACACAATTGCATCCCAAATACAAATTGTATTGCT
TATTCATTATAGCTATTCGTCCTGTAATCTGTTTCTAGGTGAAGCATACTCCAGTGTTTT
AGGGGTTTTGAAAATAAATATTTAAATTTTCACAGTCAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAA

SEQ ID NO: 2 STLK3 HUMAN

GACAGCAGCGCCGGCCCCGGCAGCTCCCGCGGCCCCGGCCCCGGCCCCGGCCCCGGCCCC
GGCGGCACAGGETGTGCGCTGGCCCATCTGCAGGGACGCGTACGAGCTGCAGGAGGTTAT
CGGCAGTGGAGCTACTGCTGTGGTTCAGGCAGCCCTATGCAAACCCAGGCAAGAACGTGT
AGCAATAAAACGGATCAACTTGGA AAAATGCCAGACCAGTATGGATGAACTATTAAAAGA
AATTCAAGCCATGAGTCAGTGCAGCCATCCCAACGTAGTGACCTATTACACCTCTTTTGT
GGTCAAAGATGAACTTTGGCTGGTCATGAAATTACTAAGTGGAGGTTCAATGTTGGATAT
CATAAAATACATTGTCAACCGAGGAGAACACAAGAATGGAGTTCTGGAAGAGGCAATAAT
AGCAACAATTCTTAAAGAGGTTTTTGAAGGCTTAGACTATCTACACAGAAACGGTCAGAT
TCACAGGGATTTGAAAGCTGGTAATATTCTTCTGGGTGAGGATGGTTCAGTACAAATAGC
AGATTTTGGGGTAAGTGC GTTCCTAGCAACAGGGGGTGATGTTACCCGAAATAAAGTAAG
AAAAACATTTCGTTGGCACCCCATGTTGGATGGCTCCTGAAGTCATGGAACAGGTGAGAGG
CTATGACTTCAAGGCTGACATGTGGAGTTTTTGAATAACTGCCATTGAATTAGCAACAGG
AGCAGCGCCTTATCACAAATATCCTCCCATGAAAGTGTTAATGTTGACTTTGCAAAATGA
TCCACCCACTTTGGAACAGGGGTAGAGGATAAAGAAATGATGAAAAAGTACGGCAAGTC
CTTTAGAAAATTACTTTCACTGTGTCTTCAGAAAGATCCTTCCAAAAGGCCACAGCAGC
AGAACTTTTAAAATGCAAATCTTCCAGAAAGCCAAGAACAGAGAGTACCTGATTGAGAA
GCTGCTTACAAGAACACCAGACATAGCCCAAAGAGCCAAAAAGGTAAGAAGAGTTCCTGG

Fig. 9B

GTCAAGTGGTCACCTTCATAAAACCGAAGACGGGGACTGGGAGTGGAGTGACGACGAGAT
GGATGAGAAGAGCGAAGAAGGGAAAGCAGCTTTTTCTCAGGAAAAGTCACGAAGAGTAAA
AGAAGAAAATCCAGAGATTGCAGTGAGTGCCAGCACCATCCCCGAACAAATACAGTCCCT
CTCTGTGCACGACTCTCAGGGCCCCACCCAATGCTAATGAAGACTACAGAGAAGCTTCTTC
TTGTGCCGTGAACCTCGTTTTGAGATTAAGAACTCCAGAAAGGAACTTAATGACATACG
ATTTGAGTTTACTCCAGGAAGAGATACAGCAGATGGTGTATCTCAGGAGCTCTTCTCTGC
TGGCTTGGTGGATGGTCACGATGTAGTTATAGTGGCTGCTAATTTACAGAAGATTGTAGA
TGATCCCAAAGCTTTAAAAACATTGACATTTAAGTTGGCTTCTGGCTGTGATGGGTCGGA
GATTCCTGATGAAGTGAAGCTGATTGGGTTTGCTCAGTTGAGTGTGAGCTGATGTATGTC
CCTTGATGTCACCCTGATCTGTCATGCCCCACCGCCACCCCTACTCCCTTCAACCCTCCC
TCTTTCTGCCCCATTTCTCTCCACCCCTCACTCCCATTTCTTAGCAAAATCAGAAGATTG
TGAAGAGGGCCGGCTTCAACAAAATGGGATAAAAAAATAATTTTTTAAACTTACAACACT
CCGAGTTCTGCTTTATTCTCTAGCAATCCACAGTACAAGAACAAGCAAATGCCACAGCTG
CACGACTGTTGCTCATTTTTTCCAAAAGCTATTTAATATTCTTAGCAATCAATTTGGATAT
CCCTTAAGTGAAAAGAATCTGAAATACACTCAGGTGGTCTTATTTATTGGCAACAAAAGG
AATTTTCTATCCAGAAGCCTATTTCTCCTTTTCAATTGTTGTTATTTCTGTTATAATACTTT
AATTGTACATCTGACAATACTGCCTCTTTTTATGTTGTATTTAGAAATTAATATACTTATA
AAATTAAGATTTATTAGCCAAACTTGAATTCTAGTTTTAAACTGACTGTGAATTTTATT
TTTCATATATTTATGCATTACACACCTTAGCTATAAGAAAAAAAGGGTTTTGATTATATG
CTTCTTGCAAGTTAATCTCGTTATTTAAACAAAAAGTTTTGGGTCTATCTTTGGAGTATTT
GTAACCTCTAAATTTTGAAATGACTGAATTAGGAATTTGGATGCTTATTCTTTTAGTCTG
TTTGCCTAAAAACCAATTTACAATCTGACTGTCTCTTGGGAGAGGGAGGTGCCTTGCAAA
CTTTCACATTAAGAATGTGCCTGAGGCTGCTTTACTCTGGAATAGTCTCAGATCTAAAT
TTCCTCTATATAAGGTGGCATATGTTAAGTTTTGCTTCATTGGACCGTTTAGAATGCTAT
GTAAAATGTTGCCATTCTGTTAGATTGCTAACTATATACCCATCTCTGATTTGGCTCTCC
TTAAGTGATAGGATTTGTTATTCTAAAGGTGATAAACTTGAAAATATCAGAATCTGAGTT
TTACTTGAAATTTTGCAGAATACCCAGGTGGAGTGAAAATTGGAAGGGTTTTGTGCAATG
ACTAAAAGGTAAAACGCTGTTAAGGTTCAAGAATCAATACTTTCAACCCAAGTAGCCCTC
TGCTTGACTGTATATTATGGAAGTAGTAAACCTTAGGATTTTGAAAATTGGAGTCTAATC
TTTCAAGGAGGTGGGCTCCAGGATGGTACCATTGCTCTTTCTAGCTAACCTAGATAT
GGCAGCTCTTTAATGTACTTCAAAAAGCAAATATATATTACTAAGGAAAAAAAGTTATTT
ATAATTGCCTTGTCATAATTGTTAAGGTGTTCTAGAGCCATTTGCATACAATTTAATGTA
ATTTCAATTCCATTCTATTGTTTACACAACGATTACTCGAAGATGACTGCAAAGGTAAAAG
GAAAATAAAAGTGTATTGCACAATGAAAAA

SEQ ID NO: 3 STLK4 HUMAN

CAAAAGTGGAGTCCTAGATGANTCTACCATTGCTACGATACTCCGAGAAGTACTGGAAGG
GCTGGAATATCTGCATAAAANTGGACAGATCCACAGAGATGTGAAAGCTGGAAACATTCT

Fig. 9C
35/76

TNTTGGAGAAGATGGCTCAGTACAGATTTTCAGACTTTGGGGTTAGTGCTTTTTTTAGCAAC
TGGTGGTGATATTACCCGAAATAAAGTGAGAAAGACCTTTGTTGGCACCCCTTGTTGGAT
GGCACCTGAAGTTATGGAACAGGTCCGTGGTTATGATTTCAAAGCTGATATTTGGAGTTT
TGGAATTACAGCAATTGAATTGGCTACAGGGGCGGCTCCTTATCATAAATATCCACCAAT
GAAGGTTTTAATGCTGACACTGCAGAACGATCCTCCTTCTTTGGAAACTGGTGTTCAAGA
TAAAGAAATGCTGAAAAAATATGGAAAATCATTTAGAAAAATGATTTTCATTGTGCCTTCA
AAAAGATCCAGAAAAAAGACCAACAGCAGCAGAACTATTAAGGCACAAATTTTTCCAGAA
AGCAAAGAATAAAGAATTTCTTCAAGAAAAAACATTGCAGAGAGCACCAACCATTTCTGA
AAGAGCAAAAAAGGTTCCGGAGAGTACCAGGTTCCAGTGGGCGTCTTCATAAGACAGAGGA
TGGAGGCTGGGAGTGGAGTGATGATGAATTTGATGAAGAAAGTGAGGAAGGGAAAGCAGC
AATTTCACTACTCAGGTCTCCCCGAGTGAAAGAATCAATATCAAATTCTGAGCTCTTTCC
AACAACTGATCCTGTGGGTACTTTGCTCCAAGTTCCAGAACAGATCTCTGCTCATCTACC
TCAGCCAGCTGGGCAGATTGCTACACAGCCAACTCAAGTCTCTCTCCCACCCACCGCAGA
GCCAGCAAAAAACAGCTCAGGCTTTGTCTTCAGGATCAGGTTCAACAAGAAACCAAGATCCC
AATCAGTCTAGTACTAAGATTAAGGAATTCCAAAAAAGAACTAAATGATATTCGATTTGA
ATTTACTCCTGGGAGAGATACAGCAGAGGGTGTCTCTCAGGAACTCATTTCTGCTGGCCT
GGTCGACGGAAGGGATTTAGTAATAGTGGCAGCTAATTTGCAGAAAATTGTGGAAGAACC
TCAGTCAAATCGATCTGTCACTTTCAAAGTGGCATCTGGTGTGGAAGGCTCAGATATTCC
TGATGATGGTAAACTGATAGGATTTGCCCAGCTCAGCATCAGCTAAACCACAACCCTGGA
AGAGGCGGCCTAAGGAGATTCCACACATGCGTATCTCTGTTGCTTCTATTGGCCTAAACC
CACTACTGCCAAAGAACCAGCAACAAACCTCCCGGCTAGGAGCTTTAGAAGTCTTTATG
TTCTTCCTGCCATCATTCTCTCTTTTCCACAGGGAAAGAAAAGTTGGATCACTAGTGGC
CAGCATCCCCAGAGTTCCGTTAGTAACTTACTTCATATGTCCCCTGTCTTCTCTCATCT
GAGAAGTGGCCCATGTGCTTCAAGGCCAGGAGGGAGATCTGTCAGCTCATTCTTGCCTT
ACTCCAATGATGGCCCAGGTGGAAAAGTAGCAGCTGTATCGGGCTTCTCATCCTGCCTG
TTCCCCCACACCTGCCAGGATATGGACATCTTGGGATATCTCTTTACCACTGAAGTAGAA
TTGATTGTTTCACTGGAGCCCAGAGAATTTAATTTAATGTTTTTTCTTTGTACCTGATGT
GAATTCTAGCAACCTTTGTTAGGAAAAAGCACAGCCTCAGATGGAGGCAGCCTAAACTGT
GTTCTTGTTTTGTTTCAATGGTGTCTTAAGCGTTTTTGCTGAAGCTGCTCTCAGGCACCCCC
TTCTTCATTGCTCTCTCCAGAAAGGGTTGCTAGCCTTAACCTTCAGCTGGTGCAAAACATC
TGAAGTGTAGCCGAACCTTCAGCCATCAGATCCTTCAAAGTGGAACCTTTGGATTGTTTTTAC
AGACAACATCGAGTAATGGCTTGTAATGTGAATTTTGCCAGAGGTGGTTTTTGAACAGG
AAAATCATAATTCATATCATTGGAGAAGTATTTATTTTCAAATATCAAATTGAAGAAAAA
CTCAATCCTCCCATGAAAATCAGTTCGCCTGGCCTCCAAGTCGTGAGGAAATGGGTATGC
AAGGCTGAGATTTCTACAGCAATAAAGGAGACACACACTGGGCCAGAGAGGCCTGCCTTC
TGCCTGCTCTCCTGCACTGACCCTTTGGAGGGGGTCTCTGTGTGCTGAAGCTAACTCAAG
ATGGAAAGTGAAACCACATGTGCCGTGACCTTTAGGTTTTATGAGTAGACAGTGTTTATT
TGATTTTCTACAGAAATAATATAAATTATTCTTTAGGTTTAAAAAAGAGCACTCATAATG

Fig. 9D

36/76

CAATATGTGAATAATCAGTGAGGTTGATTTTTCTTTTTTCTACCGTTTCATAGTCTTTG
TCTAACTGCTAGTAACCTACCGAGTTTTATATATGAGTGGGATACTCAATCTGGCCTTA
AAAAGATACACAAAGATGGGCTGTGGGTCCCTGGAAAGGGGGAGAGTTGCCCTTTACAGA
ATCACTCGAGCCCTTTCCAGCACTGTTGGTCTGATGAACAAGGTTGTTTTACCTTATTTT
CTCTTGGAACATATCTGAAAACCTTCCCCACAAATAACTTGTACACCTTTTGTTCATT
CTGAGTCTTTAGTTTTAGTCATGGGCTTTCTTCACCTGCTCTAGGTGCAAAGGCATGTTG
GGAAAGAGATGGATGTTGGGGAGGAAGAGAGGAGATGGATTTTCAGTTGGGAGTTAGGAGG
AGAGTAGGTGAGATGATCAGACACCGGAGTTCAACGTCCCAGCAGTCTTGGTAAAAGGAG
GGAGCCTGCTGAGCCAGGAGGGAGAAAAGAAGATTGACCAGCTTGCTAGAAAAATACTTA
GCTTTTCTTTTTCTTTTTTTTGTGGAGGGGGGACGGAGAGGAACAAGGATGGGGAGGTAGG
AATGAGGTATAGAAAAGAGATAGCATCTTCTTTGGCACAAGACTAGTGGCTTACCGCTTA
CCTTAGAGTTTTTGTTTTTTTTTTTTCAAACCCATCAAAATCTACTTATTTATGAATCCAA
GGGGTGGCAGCATCACTCTGTTCTAGCATTCTTTGTGGAGATGGTCTGGTGCCTAGCTGG
GAGTGAGCAGCAGCCCATCCCCTGTTCACTTTCTCTAGCCCATCATTACCTGTGAACTGC
AGTGGGGCAGTCATGGCAAATAGAATTGGGCTGGGGTTTCTCCTTCTTTTCAGTTCATTG
TTTGGCCTGCTAGGAATTAGAAGACAGACACCATGTCCCAGGACAGTGTTACTTCTTCTG
CATGATGTGTGGTAGACTCCCTTTGCTGGCTTGTGCAGTGATACTGAGAAAATACATGAA
CAGAAACTGCCCAGGTGGAACAGCACGTAACCTAGTGAGTGACTGTACTCCTTTCTAGGA
ATGCTGATTCAGAGTGCACCTCTTTGACTAGGTCCCAGGATCCCCTTGTCCCTGGAGTAG
GGACTAACTATAGCACAAAGTAATATGTGCCAATGCTATTTGTGAAATGTTTGGTCTTTC
TAAACGACTAAAGGATTTGTTGGGTTTTTGTCTTAAGTTTTGAACCAAATCCTAGAGCCAG
CTGATAATATTTAATAATCTGGAGGAGAGAATAATGATGTACCAATAAGTGGAGATTCCT
CCTTATGATGTATGCTAGGTTATGGAAGATGTAAAATATTCAACTTTTTCTCCTTTTTT
TGGACTTTGTATTTTACTGCATGTTTTCTTCATTTTTAATCAATAAAGAGTAAATTGTCA
AAAAAAAAAAAAAAAAAAAA

SEQ ID NO: 4 STLK5 HUMAN

CTCATCTGTACACACTTCATGGATGGCATGAATGAGCTGGCGATTGCTTACATCCTGCAG
GGGGTGCTGAAGGCCCTCGACTACATCCACCACATGGGATATGTACACAGGAGTGTCAA
GCCAGCCACATCCTGATCTCTGTGGATGGGAAGGTCTACCTGTCTGGTTTGGCGAGCAAC
CTCAGCATGATAAGCCATGGGCAGCGGCAGCGAGTGGTCCACGATTTTCCCAAGTACAGT
GTCAAGGTTCTGCCGTGGCTCAGCCCCGAGGTCCTCCAGCAGAATCTCCAGGGTTATGAT
GCCAAGTCTGACATCTACAGTGTGGGAATCACAGCCTGTGAACTGGCCAACGGCCATGTC
CCCTTTAAGGATATGCCTGCCACCCAGATGCTGCTAGAGAACTGAACGGCACAGTGCCC
TGCCTGTTGGATAACCAGCACCATCCCCGCTGAGGAGCTGACCATGAGCCCTTCGCGCTCA
GTGGCCAACCTCTGGCCTGAGTGACAGCCTGACCACCAGCACCCCCCGGCCCTCCAACGGT
GACTCGCCCTCCCACCCCTACCACCGAACCTTCTCCCCCACTTCCACCACTTTGTGGAG
CAGTGCCTTCAGCGCAACCCGGATGCCAGGCCAGTGCCAGCACCTCCTGAACCACTCT

Fig. 9E
37/76

TTCTTCAAGCAGATCAAGCGACGTGCCTCAGAGGCTTTGCCCGAATTGCTTCGTCCTGT
ACCCCCATCACCAATTTTGAGGGCAGCCAGTCTCAGGACCACAGTGGAAATCTTTGGCCTG
GTAACAAACCTGGAAGAGCTGGAGGTGGACGATTGGGAGTTCTGAGCCTCTGCAAACCTGT
GCGCATTCTCCAGCCAGGGATGCAGAGGGCCACCCAGAGGCCCTTCCTGAGGGCCGGCCAC
ATTCCCGCCCTCCTGGGCAGATTGGGTAGAAAGGACATTCTTCCAGGAAAGTTGACTGCT
GACTGATTGGGAAAGAAAATCCTGGAGAGATACTTCACTGCTCCAAGGCTTTTGAGACAC
AAGGGAATCTCAACAACCAGGGATCAGGAGGGTCCAAAGCCGACATTCCCAGTCCTGTGA
GCTCAGGTGACCTCCTCCGCAGAAGAGAGATGCTGCTCTGGCCCTGGGAGCTGAATTCCA
AGCCCAGGGTTTGGCTCCTTAAACCCGAGGACCGCCACCTCTTCCCAGTGCTTGCGACCA
GCCTCATTCTATTTAACTTTGCTCTCAGATGCCTCAGATGCTATAGGTCAGTGAAAGGGC
AAGTAGTAAGCTGCCTGCCTCCCTTCCCTCAGACCTCTCCCTCATAATTCCAGAGAAGGG
CATTTCTGTCTTTTTTAAGCACAGACTAAGGCTGGAACAGTECATCCTTATCCCTCTTCTG
GCTTGGGCCCTGACACCTAAGTCTTTCCACGGTTTATGTGTGTGCCTCATTCTTTCCC
ACCAAGAATCCATCTTAGCGCCTCCTGCCAGCTGCCCTGGTGCTTTCTCCAAGGGCCATC
AGTGTCTTGCCTAGCTTGAGGGCTTAAGTCCTTATGCTGTGTTAGTTTCGTTGTCAGAAC
AAATTAATAATTTTCAGAGACGCTG

SEQ ID NO: 9 ZC1 HUMAN

GAGACCATGGCGAACGACTCTCCCGCGAAAAGTCTGGTGGACATCGACCTCTCCTCCCTG
CGGGATCCTGCTGGGATTTTTGAGCTGGTGGAAAGTGGTTGGAAATGGCACCTATGGACAA
GTCTATAAGGGTCGACATGTTAAAACGGGTCAGTTGGCAGCCATCAAAGTTATGGATGTC
ACTGAGGATGAAGAGGAAGAAATCAAACCTGGAGATAAATATGCTAAAGAAATACTCTCAT
CACAGAAACATTGCAACATATTATGGTGCTTTTCATCAAAAAGAGCCCTCCAGGACATGAT
GACCAACTCTGGCTTGTTATGGAGTTCTGTGGGGCTGGGTCCATTACAGACCTTGTTGAAG
AACACCAAAGGGAACACACTCAAAGAAGACTGGATCGCTTACATCTCCAGAGAAATCCTG
AGGGGACTGGCACATCTTCACATTCATCATGTGATTCAACGGGATATCAAGGGCCAGAAT
GTGTTGCTGACTGAGAATGCAGAGGTGAAACTTGTTGACTTTGGTGTGAGTGCTCAGCTG
GACAGGACTGTGGGGCGGAGAAATACGTTTCATAGGCACTCCCTACTGGATGGCTCCTGAG
GTCATCGCCTGTGATGAGAACCCAGATGCCACCTATGATTACAGAAGTGATCTTTGGTCT
TGTGGCATTACAGCCATTGAGATGGCAGAAGGTGCTCCCCCTCTCTGTGACATGCATCCA
ATGAGAGCACTGTTTTCTCATTCCCAGAAACCTCCTCCCCGGCTGAAGTCAAAAAAATGG
TCGAAGAAGTTTTTTAGTTTTATAGAAGGGTGCCTGGTGAAGAATTACATGCAGCGGGCC
TCTACAGAGCAGCTTTTGAAACATCCTTTTATAAGGGATCAGCCAAATGAAAGGCAAGTT
AGAATCCAGCTTAAGGATCATATAGATCGTACCAGGAAGAAGAGAGGGCGAGAAAGATGAA
ACTGAGTATGAGTACAGTGGGAGTGAGGAAGAAGAGGAGGAAGTGCTGAACAGGAAGGA
GAGCCAAGTTCCATTGTGAACGTGCCTGGTGAAGTCTACTCTTCGCCGAGATTTCTGAGA
CTGCAGCAGGAGAACAAGGAACGTTCCGAGGGCTCTTCGGAGACAACAGTTACTACAGGAG
CAACAGCTCCGGGAGCAGGAAGAATATAAAAGGCAACTGCTGGCAGAGAGACAGAAGCGG

Fig. 9F
38/76

ATTGAGCAGCAGAAAGAACAGAGGCGACGGCTAGAAGAGCAACAAAGGAGAGAGCGGGAA
GCTAGAAGGCAGCAGGAACGTGAACAGCGAAGGAGAGAACAAGAAGAAAAGAGGGCGTCTA
GAGGAGTTGGAGAGAAGGCGCAAAGAAGAAGAGGAGAGGAGACGGGCAGAAGAAGAAAAG
AGGAGAGTTGAAAGAGAACAGGAGTATATCAGGCGACAGCTAGAAGAGGAGCAGCGGCAC
TTGGAAGTCCTTCAGCAGCAGCTGCTCCAGGAGCAGGCCATGTTACTGGAGTGCCGATGG
CGGGAGATGGAGGAGCACCGGCAGGCAGAGAGGCTCCAGAGGCAGTTGCAACAAGAACAA
GCATATCTCCTGTCTCTACAGCATGACCATAGGAGGGCCGCACCCGCAGCACTCGCAGCAG
CCGCCACCACCGCAGCAGGAAAGGAGCAAGCCAAGCTTCCATGCTCCCGAGCCCCAAAGCC
CACTACGAGCCTGCTGACCGAGCGCGAGAGGTGGAAGATAGATTTAGGAAAATAACCAC
AGCTCCCCTGAAGCCCAGTCTAAGCAGACAGGCAGAGTATTGGAGCCACCAGTGCCTTCC
CGATCAGAGTCTTTTTCCAATGGCAACTCCGAGTCTGTGCATCCCGCCCTGCAGAGACCA
GCGGAGCCACAGGTTCTCTGTGAGAACAAACATCTCGCTCCCCTGTTCTGTCCCGTCGAGAT
TCCCCACTGCAGGGGCAGTGGGCAGCAGAATAGCCAGGCAGGACAGAGAACTCCACCAGT
ATTGAGCCCAGGCTTCTGTGGGAGAGAGTGGAGAAGCTGGTGCCCAGACCTGGCAGTGGC
AGCTCCTCAGGGTCCAGCAACTCAGGATCCCAGCCCCGGGTCTCACCTGGGTCTCAGAGT
GGCTCCGGGGAAACGCTTCAGAGTGAGATCATCATCCAAGTCTGAAGGCTCTCCATCTCAG
CGCCTGGAAAATGCAGTGAAAAAACCTGAAGATAAAAAGGAAGTTTTTCAGACCCCTCAAG
CCTGCTGATCTGACCGCACTGGCCAAAGAGCTTCGAGCAGTGGAAGATGTACGGCCACCT
CACAAAGTAACGGACTACTCCTCATCCAGTGAGGAGTCGGGGACGACGGATGAGGAGGAC
GACGATGTGGAGCAGGAAGGGGCTGACGAGTCCACCTCAGGACCAGAGGACACCAGAGCA
GCGTCATCTCTGAATTTGAGCAATGGTGAAACGGAATCTGTGAAAACCATGATTGTCCAT
GATGATGTAGAAAGTGAGCCGGCCATGACCCCATCCAAGGAGGGCACTCTAATCGTCCGC
CGGACTCAGTCCGCTAGTAGCACACTCCAGAAACACAAATCTTCCTCCTCCTTTACACCT
TTTATAGACCCCAGATTACTACAGATTTCTCCATCTAGCGGAACAACAGTGACATCTGTG
GTGGGATTTTCTGTGATGGGATGAGACCAGAAGCCATAAGGCAAGATCCTACCCGGAAA
GGCTCAGTGGTCAATGTGAATCCTACCAACACTAGGCCACAGAGTGACACCCCGGAGATT
CGTAAATACAAGAAGAGGTTTAACTCTGAGATTCTGTGTGCTGCCTTATGGGGAGTGAAT
TTGCTAGTGGGTACAGAGAGTGGCCTGATGCTGCTGGACAGAAGTGGCCAAGGGAAGGTC
TATCCTCTTATCAACCGAAGACGATTTCAACAAATGGACGTACTTGAGGGCTTGAATGTC
TTGGTGACAATATCTGGCAAAAAGGATAAGTTACGTGTCTACTATTTGTCTGTTAAGA
AATAAAATACTTCACAATGATCCAGAAGTTGAGAAGAAGCAGGGATGGACAACCGTAGGG
GATTTGGAAGGATGTGTACATTATAAAGTTGTAAAATATGAAAGAATCAAATTTCTGGTG
ATTGCTTTGAAGAGTTCTGTGGAAGTCTATGCGTGGGCACCAAAGCCATATCACAAATTT
ATGGCCTTTAAGTCATTTGGAGAATTGGTACATAAGCCATTACTGGTGGATCTCACTGTT
GAGGAAGGCCAGAGGTTGAAAGTGATCTATGGATCCTGTGCTGGATTCCATGCTGTTGAT
GTGGATTCAGGATCAGTCTATGACATTTATCTACCAACACATATCCAGTGTAGCATCAAA
CCCCATGCAATCATCATCCTCCCCAATACAGATGGAATGGAGCTTCTGGTGTGCTATGAA
GATGAGGGGGTTTATGTAAACACATATGGAAGGATCACCAAGGATGTAGTTCTACAGTGG

Fig. 9G

39/76

GGAGAGATGCCTACATCAGTAGCATATATTCGATCCAATCAGACAATGGGCTGGGGAGAG
AAGGCCATAGAGATCCGATCTGTGGAACTGGTCACTTGGATGGTGTGTTTCATGCACAAA
AGGGCTCAAAGACTAAAATTCTTGTGTGAACGCAATGACAAGGTGTTCTTTGCCTCTGTT
CGGTCTGGTGGCAGCAGTCAGGTTTATTTTCATGACCTTAGGCAGGACTTCTCTTCTGAGC
TGGTAGAAGCAGTGTGATCCAGGGATTACTGGCCTCCAGAGTCTTCAAGATCCTGAGAAC
TTGGAATTCCTTGTAAC

SEQ ID NO: 10 ZC2 HUMAN

GCTTTCGGGGAGGTCTATGAGGGTCGTCATGTCAAAACGGGCCAGCTTGCAGCCATCAAG
GTTATGGATGTCACAGGGGATGAAGAGGAAGAAATCAAACAAGAAATTAACATGTTGAAG
AAATATTCTCATCACCGGAATATTGCTACATACTATGGTGTCTTTTATCAAAAAGAACCCA
CCAGGCATGGATGACCAACTTTGGTTGGTGATGGAGTTTTGTGGTGCTGGCTCTGTCACC
GACCTGATCAAGAACACAAAAGGTAACACGTTGAAAGAGGAGTGGATTGCATACATCTGC
AGGGAAATCTTACGGGGGCTGAGTCACCTGCACCAGCATAAAGTGATTTCATCGAGATATT
AAAGGGCAAAATGTCTTGCTGACTGAAAATGCAGAAGTTAACTAGTGGACTTTGGAGTC
AGTGCTCAGCTTGATCGAACAGTGGGCAGGAGGAATACTTTTCATTGGAACCTCCTACTGG
ATGGCACCAGAAGTTATTGCCTGTGATGAAAACCCAGATGCCACATATGATTTCAAGAGT
GACTTGTGGTCTTTGGGTATCACCGCCATTGAAATGGCAGAAGGTGCTCCCCCTCTCTGT
GACATGCACCCCATGAGAGCTCTCTTCCTCATCCCCCGGAATCCAGCGCCTCGGCTGAAG
TCTAAGAAGTGGTCAAAAAAATTCCAGTCATTTATTGAGAGCTGCTTGGTAAAGAATCAC
AGCCAGCGACCAGCAACAGAACAATTGATGAAGCATCCATTTATACGAGACCAACCTAAT
GAGCGACAGGTCCGCATTCAACTCAAGGACCATATTGATAGAACAAGAAAGAGCGAGGA
GAAAAAGATGAGACAGAGTATGAGTACAGTGGAGGTGAGGAAGAAGAGGAGGAGAATGAC
TCAGGAGAGCCCAGCTCCATCCTGAATCTGCCAAGGGAGTCGACGCTGCGGAGGGACTTT
CTGAGGCTGCAGCTGGCCAACAAGGAGCGTTCTGAGGCCCTACGGAGGCAGCAGCTGGAG
CAGCAGCAGCGGGAGAATGAGGAGCACAAGCGGCAGCTGCTGGCCGAGCGTCAGAAGCGC
ATCGAGGAGCAGAAAGAGCAGAGGCGGCGGCTGGAGGAGCAACAAGGCGAGAGAAGGAG
CTGCGGAAGCAGCAGGAGAGGGAGCAGCGCCGGCACTATGAGGAGCAGATGCGCCGGGAG
GAGGAGAGGAGGCGTGCGGAGCATGAACAGGAATATAAGCGCAAACAATTGGAAGAACAG
AGACAAGCAGAAAGACTGCAGAGGCAGCTAAAGCAAGAAAGAGACTACTTAGTTTTCCCTT
CAGCATCAGCGGCAGGAGCAGAGGCCTGTGGAGAAGAAGCCACTGTACCATTACAAGAA
GGAATGAGTCCTAGTGAGAAGCCAGCATGGGCCAAGGAGGTAGAAGAACGGTCAAGGCTC
AACCGGCAAGTTCCCCTGCCATGCCTCACAAGGTTGCCAACAGGATATCTGACCCCAAC
CTGCCCCCAAGGTCGGAGTCCTTCAGCATTAGTGGAGTTCAGCCTGCTCGAACACCCCCC
ATGCTCAGACCAGTCGATCCCCAGATCCCACATCTGGTAGCTGTAAAATCCCAGGGACCT
GCCTTGACCGCCTCCAGTCAGTGCACGAGCAGCCCACAAAGGGCCTCTCTGGGTTTCAG
GAGGCTCTGAACGTGACCTCCACCGCGTGGAGATGCCACGCCAGAAGCTCAGATCCCACC
TCGGAAAATCCTCCTCTCCCCACTCGCATTGAAAAGTTTGACCGAAGCTCTTGGTTACGA

CAGGAAGAAGACATTCCACCAAAGGTGCCTCAAAGAACAACCTTCTATATCCCCAGCATTAGCCAGAAAGAATTCTCCTGGGAATGGTAGTGCTCTGGGACCCAGACTAGGATCTCAACCCATCAGAGCAAGCAACCCTGATCTCCGGAGAACTGAGCCCATCTTGAGAGAGCCCCTTGAGAGGACCAGCAGTGGCAGTTCCTCCAGCTCCAGCACCCCTAGCTCCCAGCCCAGCTCCCAAAGGAGCTCCCAGCCTGGATCACAAAGCAGGATCCAGTGAACGCACCAGAGTTCGAGCCAAACAGTAAGTCAGAAGGATCACCTGTGCTCCCCCATGAGCCTGCCAAGGTGAAACCAGAAGAAATCCAGGGACATTACCCGGCCCCAGTCGACCAGCTAGCTACAAAAAAGCTATAGATGAGGATCTGACGGCATTAGCCAAAGAACTAAGAGAACTCCGGATTGAAGAAACAAACCGCCCAATGAAGAAGGTGACTGATTACTCCTCCTCCAGTGAGGAGTCAGAAAGTAGCGAGGAAGAGGGAGGAAGATGGAGAGAGCGAGACCCATGATGGGACAGTGGCTGTCAGCGACATACCCAGACTGATACCAACAGGAGCTCCAGGCAGCAACGAGCAGTACAATGTGGGAATGGTGGGGACGCATGGGCTGGAGACCTCTCATGCGGACAGTTTCAGCGGCAGTATTTCAAGAGAAGGAACCTTGATGATTAGAGAGACGTCTGGAGAGAAGAAGCGATCTGGCCACAGTGACAGCAATGGCTTGGCTGGCCACATCAACCTCCCTGACCTGGTGCAGCAGAGCCATTCTCCAGCTGGAACCCCGACTGAGGGACTGGGGCGCGTCTCAACCCATTCCCAGGAGATGGACTCTGGGACTGAATATGGCATGGGGAGCAGCAACCAAAGCCTCCTTCACCCCTTTGTGGACCCAGAGTATACCAAGACGTCTCCCCTGATGAAGATGAAGAGGATGAGGAATCATCAGCCGCAGCTCTGTTTACTGGCGAACTTCTTAGGCAAGAACAGGGCCAACTCAATGAAGCAAGAAAGATTTGCGGTGGTAATGTAAACCCAACCAACATTTCGGCCTCATAGCGACACACCAGAAATCAGAAAATACAAGAAACGATTCAACTCAGAAATACTTTGTGCAGCTCTGTGGGGTGTAACCTTCTGGTGGGGACTGAAAATGGCCTGATGCTTTTTGGACCGAAGTGGGCAAGGCAAAGTCTATAATCTGATCAACCGGAGGCGATTTTCAGCAGATGGATGTGCTAGAGGGACTGAATGTCCTTGTGACAATTTCAGGAAAGAAGAATAAGCTACGAGTTTACTATCTTTCATGGTTAAGAAACAGAATACTACATAATGACCCAGAAGTAGAAAAGAAACAAGGCTGGATCACTGTTGGGGACTTGGAAGGCTGTATACATTATAAAGTTGTTAAATATGAAAGGATCAAATTTTTGGTGATTGCCTTAAAGAATGCTGTGGAAATATATGCTTGGGCTCCTAAACCGTATCATAAATTCATGGCATTTAAGTCTTTTGCAGATCTCCAGCACAAAGCCTCTGCTAGTTGATCTCACGGTAGAAGAAGGTCAAAGATTAAAGGTTATTTTTGGTTCACACACTGGTTTCCATGTAATTGATGTTGATTCAGGAACCTCTTATGATATCTACACACCATCTCATATTCAGGGCAATATCACTCCTCATGCTATTGTCATCTTGCCTAAAACAGATGGAATGGAAATGCTTGTTTGCTATGAGGATGAGGGGGTGATGTAAACACCTATGGCCGGATAACTAAGGATGTGGTGCTCCAATGGGGAGAAATGCCCACGTCTGTGGCCTACATTCATTCCAATCAGATAATGGGCTGGGGCGAGAAAGCTATTGAGATCCGGTCAGTGGAAACAGGACATTTGGATGGAGTATTTATGCATAAGCGAGCTCAAAGGTTAAAGTTTCTATGTGAAAGAAATGATAAGGTATTTTTTGCATCCGTGCGATCTGGAGGAAGTAGCCAAGTGTTTTTTCATGACCCTCAACAGAAATTCATGATGAACTGGTAACAGAAGAGCACTTGGCACTTATCTTCATGGCGTTATTTCTAATTTAAAGAACATAACTCATGTGGACTTATGCCAGTCTAGAGGCAGAATCAGAAGGCTTGGTTGAACATATCGCTTTCCTTTTTCCTCTCCCTCCGCCCCCTCCCAGTACAGTCCATCT

Fig. 9 I
41/76

SEQ ID NO: 11 ZC3 HUMAN

GCATTTGGGGAGGTGTATGAGGGTCGGCATGTCAAGACGGGGCAGCTGGCTGCCATCAAG
GTCATGGATGTCACGGAGGACGAGGAGGAAGAGATCAAACAGGAGATCAACATGCTGAAA
AAGTACTCTCACCACCGCAACATCGCCACCTACTACGGAGCCTTCATCAAGAAGAGCCCC
CCGGGAAACGATGACCAGCTCTGGCTGGTGTATGGAGTTCTGTGGTGCTGGTTCAGTGACT
GACCTGGTAAAGAACACAAAAGGCAACGCCCTGAAGGAGGACTGTATCGCCTATATCTGC
AGGGAGATCCTCAGGGGTCTGGCCCATCTCCATGCCCCACAAGGTGATCCATCGAGACATC
AAGGGGCAGAATGTGCTGCTGACAGAGAATGCTGAGGTCAAGCTAGTGGATTTTGGGGTG
AGTGCTCAGCTGGACCGCACCGTGGGCAGACGGAACACTTTCATTGGGACTCCCTACTGG
ATGGCTCCAGAGGTCATCGCCTGTGATGAGAACCCTGATGCCACCTATGATTACAGGAGT
GATATTTGGTCTCTAGGAATCACAGCCATCGAGATGGCAGAGGGAGCCCCCCTCTGTGT
GACATGCACCCCATGCGAGCCCTCTTCCTCATTCCCTCGGAACCCTCCGCCCAGGCTCAAG
TCCAAGAAGTGGTCTAAGAAGTTCATTGACTTCATTGACACATGTCTCATCAAGACTTAC
CTGAGCCGCCCCACCCACGGAGCAGCTACTGAAGTTTCCCTTCATCCGGGACCAGCCCACG
GAGCGGCAGGTCCGCATCCAGCTTAAGGACCACATTGACCGATCCCGGAAGAAGCGGGGT
GAGAAAGAGGAGACAGAATATGAGTACAGCGGCAGCGAGGAGGAAGATGACAGCCATGGA
GAGGAAGGAGAGCCAAGCTCCATCATGAACGTGCCTGGAGAGTCGACTCTACGCCGGGAG
TTTCTCCGGCTCCAGCAGGAAAATAAGAGCAACTCAGAGGCTTTAAAACAGCAGCAGCAG
CTGCAGCAGCAGCAGCAGCAGACCCCGAGGCACACATCAAACACCTGCTGCACCAGCGG
CAGCGGCGCATAGAGGAGCAGAAGGAGGAGCGGCGCCGCGTGGAGGAGCAACAGCGGCGG
GAGCGGGAGCAGCGGAAGCTGCAGGAGAAGGAGCAGCAGCGGCGGCTGGAGGACATGCAG
GCTCTGCGGCGGGAGGAGGAGCGGCGGCAGGCGGAGCGCGAGCAGGAATATATTCTGCAC
AGGCTAGAGGAGGAGCAGCGACAGCTCGAGATCCTTCAGCAACAGCTGCTCCAGGAACAG
GCCCTGCTGCTGGAATACAAGCGGAAGCAGCTGGAGGAGCAGCGGCAGTCAGAACGTCTC
CAGAGGCAGCTGCAGCAGGAGCATGCCTACCTCAAGTCCCTGCAGCAGCAGCAACAGCAG
CAGCAGCTTCAGAAACAACAGCAGCAGCAGCTCCTGCCTGGGGACAGGAAGCCCCTGTAC
CATTATGGTCGGGGCATGAATCCCGCTGACAAACCAGCCTGGGCCCCGAGAGGTAGAAGAG
AGAACAAGGATGAACAAGCAGCAGAACTCTCCCTTGGCCAAGAGCAAGCCAGGCAGCACG
GGGCCTGAGCCCCCATCCCCAGGCCTCCCCAGGGCCCCCAGGACCCCTTTCCCAGACT
CCTCCTATGCAGAGGCCGGTGGAGCCCCAGGAGGGACCGCACAAAGAGCCTGGTGGCACAC
CGGGTCCCCTGAAGCCATATGCAGCACCTGTACCCCGATCCAGTCCCTGCAGGACCAG
CCCACCCGAAACCTGGCTGCCTTCCCAGCCTCCCATGACCCCGACCCTGCCATCCCCGCA
CCCCTGCCACGCCAGTGCCCGAGGAGCTGTCATCCGCCAGAATTCAGACCCCACTCT
GAAGGACCTGGCCCCAGCCCGAATCCCCAGCCTGGGTCCGCCCAGATAACGAGGCCCCA
CCCAAGGTGCCTCAGAGGACCTCATCTATCGCCACTGCCCTTAACACCAGTGGGGCCGGA
GGGTCCCGGCCAGCCCAGGCAGTCCGTGCCAGACCTCGCAGCAACTCCGCCTGGCAAATC
TATCTGCAAAGGCGGGCAGAGCGGGGCACCCCAAAGCCTCCAGGGCCCCCTGCTCAGCCC
CCTGGCCCCGCCAACGCCTCTAGTAACCCCGACCTCAGGAGGAGCGACCCTGGCTGGGAA

Fig. 9J

42/76

CGCTCGGACAGCGTCCTTCCAGCCTCTCACGGGCACCTCCCCCAGGCTGGCTCACTGGAG
CGGAACCGCGTGGGAGTCTCCTCCAAACCGGACAGCTCCCCTGTGCTCTCCCCTGGGAAT
AAAGCCAAGCCCGACGACCACCGCTCACGGCCAGGCCGGCCCGCAGACTTTGTGTTGCTG
AAAGAGCGGACTCTGGACGAGGCCCTCGGCCTCCCAAGAAGGCCATGGACTACTCGTCG
TCCAGCGAGGAGGTGGAAAGCAGTGAGGACGACGAGGAGGAAGGCCGAAGGCCGGGCCAGCA
GAGGGGAGCAGAGATACCCCTGGGGGCGCGATGGGGATACAGACAGCGTCAGCACCATG
GTGGTCCACGACGTGAGGAGATCACCGGGACCCAGCCCCCATAAGGGGGCGGCACCATG
GTGGTCCAGCGCACCCCTGAAGAGGAGCGGAACCTGCTGCATGCTGACAGCAATGGGTAC
ACAAACCTGCCTGACGTGGTCCAGCCCAGCCACTCACCCACCGAGAACAGCAAAGGCCAA
AGCCCCACCCTCGAAGGATGGGAGTGGTGACTACCAGTCTCGTGGGCTGGTAAAGGCCCT
GGCAAGAGCTCGTTCACGATGTTTGTGGATCTAGGGATCTACCAGCCTGGAGGCAGTGGG
GACAGCATCCCCATCACAGCCCTAGTGGGTGGAGAGGGGCACTCGGCTCGACCAGCTGCAG
TACGACGTGAGGAAGGGTTCTGTGGTCAACGTGAATCCCACCAACACCCGGGCCACAGT
GAGACCCCTGAGATCCGGAAGTACAAGAAGCGATTCAACTCCGAGATCCTCTGTGCAGCC
CTTTGGGGGGTCAACCTGCTGGTGGGCACGGAGAACGGGCTGATGTTGCTGGACCGAAGT
GGGCAGGGCAAGGTGTATGGACTCATTGGGCGGCGACGCTTCCAGCAGATGGATGTGCTG
GAGGGGCTCAACCTGCTCATCACCATCTCAGGGAAAAGGAACAACTGCGGGTGTATTAC
TTGTCCTGGCTCCGGAACAAGATTCTGCACAATGACCCAGAAGTGGAGAAGAAGCAGGGC
TGGACCACCGTGGGGGACATGGAGGGCTGCGGGCACTACCGTGTGTGAAATACGAGCGG
ATTAAGTTCCTGGTCATCGCCCTCAAGAGCTCCGTGGAGGTGTATGCCTGGGGCCCCAAA
CCCTACCACAAATTTCATGGCCTTCAAGTCCTTTGCCGACCTCCCCACCGCCCTCTGCTG
GTCGACCTGACAGTAGAGGAGGGGCAGCGGCTCAAGGTCATCTATGGCTCCAGTGCTGGC
TTCCATGCTGTGGATGTCGACTCGGGGAACAGCTATGACATCTACATCCCTGTGCACATC
CAGAGCCAGATCACGCCCCATGCCATCATCTTCTCCCAACACCGACGGCATGGAGATG
CTGCTGTGCTACGAGGACGAGGGTGTCTACGTCAACACGTACGGGCGCATCATTAAAGGAT
GTGGTGTGCTGCAGTGGGGGGAGATGCCTACTTCTGTGGCCTACATCTGCTCCAACCAGATA
ATGGGCTGGGGTGAGAAAGCCATTGAGATCCGCTCTGTGGAGACGGGCCACCTCGACGGG
GTCTTCATGCACAAACGAGCTCAGAGGCTCAAGTTCCTGTGTGAGCGGAATGACAAGGTG
TTTTTTGCCTCAGTCCGCTCTGGGGGCAGCAGCCAAGTTTACTTCATGACTCTGAACCGT
AACCGCATCATGAACTGGTGACGGGGCCCTGGGCTGGGGCTGTCCACACTGGACCCAGC
TCTCCCCCTGCAGCCAGGCTTCCCGGGCCGCCCTCTTTCCCTCCCTGGGCTTTTGCTT
TACTGGTTTGATTTCACTGGAGCCTGCTGGGAACGTGACCTCTGACCCCTGA

SEQ ID NO: 12 ZC4 HUMAN

CAATGTAAACCCACTCTATGTCTCTCCTGCATGTAAAAAACCACTAATCCACATGTATGA
AAAGGAGTTCACCTTCTGAGATCTGCTGTGGTTCTTTGTGGGGAGTCAATTTGCTGTTGGG
AACCCGATCTAATCTATATCTGATGGACAGAAGTGGAAGGCTGACATTACTAACTTAT
AAGGCGAAGACCATTCCGCCAGATTCAAGTCTTAGAGCCACTCAATTTGCTGATTACCAT

Fig. 9K
43/76

CTCAGGTCATAAGAACAGACTTCGGGTGTATCATCTGACCTGGTTGAGGAACAAGATTTT
GAATAATGATCCAGAAAGTAAAAGAAGGCAAGAAGAAATGCTGAAGACAGAGGAAGCCTG
CAAAGCTATTGATAAGTTAACAGGCTGTGAACACTTCAGTGTCTCTCCAACATGAAGAAAC
AACATATATTGCAATTGCTTTGAAATCATCAATTCACCTTTATGCATGGGCACCAAAGTC
CTTTGATGAAAGCACTGCTATTAAAGTATTTCCAACACTTGATCATAAGCCAGTGACAGT
TGACCTGGCTATTGGTTCTGAAAAAAGACTAAAGATTTTCTTCAGCTCAGCAGATGGATA
TCACCTCATCGATGCAGAATCTGAGGTTATGTCTGATGTGACCCTGCCAAAGAATCCCCCT
GGAAATCATTATACCACAGAATATCATCATTTTACCTGATTGCTTGGGAATTGGCATGAT
GCTCACCTTCAATGCTGAAGCCCTCTCTGTGGAAGCAAATGAACAACCTCTTCAAGAAGAT
CCTTGAAATGTGGAAAGACATACCATCTTCTATAGCTTTTGAATGTACACAGCGAACCAC
AGGATGGGGCCAAAAGGCCATTGAAGTGCGCTCTTTGCAATCCAGGGTTCTGGAAAGTGA
GCTGAAGCGCAGGTCAATTAAGAAGCTGAGATTCTGTGCACCCGGGGTGACAAGCTGTT
CTTTACCTCTACCCTGCGCAATCACCACAGCCGGGTTTACTTCATGACACTTGGAAAAC
TGAAGAGCTCCAAAGCAATTATGATGTCTAAAAGTTTCCAGTGATTTATTACCACATTAT
AAACATCATGTATAGGCAGTCTGCATCTTCAGATTTTCAGAGATTAAATGAGTATTCAGTT
TTATTTTTAGTAAAGATTAAATCCAAAACCTTTACTTTTAATGTAGCACAGAATAGTTTTA
ATGAGAAATGCAGCTTTATGTATAAAATTAAGTATAGCAAGCTCTAGGTACTCCAATGGT
GTACAATGTCTTTTGACAAACTTTGTAACCTTTTGTTACTGTGAATTCAAACATTACTCT
TTGGACAGTTTGGACAGTATCTGTATTTCAGATTTTACAACATGGAGTAAAGAAACCTGTT
ATGAATTAGATTACAAGCAGCCTTCAAAGAATTGGCACTGGGATAAGATTTTTTCAGAAA
AGAAAAACATCGGCCAACT

SEQ ID NO: 17 KHS2 HUMAN

CCGCCATGAACCCCGGCTTCGATTTGTCCCGCCGGAACCCGCAGGAGGACTTCGAGCTGA
TTCAGCGCATCGGCAGCGGCACCTACGGCGACGTCTACAAGGCACGGAATGTTAACACTG
GTGAATTAGCAGCAATTAAAGTAATAAAATTGGAACCAGGAGAAGACTTTGCAGTTGTGC
AGCAAGAAATTATTATGATGAAAGACTGTAAACACCCAAATATTGTTGCTTATTTTTGGAA
GCTATCTCAGGCGAGATAAGCTTTGGATTTGCATGGAGTTTTGTGGAGGTGGTTCTTTAC
AGGATATTTATCACGTAAGTGGACCTCTGTCAGAACTGCAAATTGCATATGTTAGCAGAG
AAACACTGCAGGGATTATATTATCTTCACAGTAAAGGAAAAATGCACAGAGATATAAAGG
GAGCTAACATTCTATTAACGGATAATGGTCATGTGAAATTGGCTGATTTTGGAGTATCTG
CACAGATAACAGCTACAATTGCCAAACGGAAGTCTTTCATTGGCACACCATATTGGATGG
CTCCAGAAGTTGCAGCTGTTGAGAGGAAGGGGGTTACAATCAACTCTGTGATCTCTGGG
CAGTGGGAATCACTGCCATAGAACTTGCAGAGCTTCAGCCTCCTATGTTTGAATTACACC
CAATGAGAGCATTATTTCTAATGACAAAAAGCAATTTTCAGCCTCCTAACTAAAGGATA
AAATGAAATGGTCAAATAGTTTTTCATCACTTTGTGAAAATGGCACTTACCAAAAATCCGA
AAAAAAGACCTACTGCTGAAAAATTATTACAGCATCCTTTTGTAAACACAACATTTGACAC
GGTCTTTGGCAATCGAGCTGTTGGATAAAGTAAATAATCCAGATCATTCCACTTACCATG

Fig. 9L
44/76

ATTTTCGATGATGATGATCCTGAGCCTCTTGTTGCTGTACCATAGAAATTCACCTCAACAA
GTAGAAACGTGAGAGAAGAAAAACACGCTCAGAGATAACCTTTGGCCAAGTGAAATTTG
ATCCACCCTTAAGAAAGGAGACAGAACCATCATGAACTTCCCGACAGTGATGGTTTTT
TGGACAGTTCAGAAGAAATATACTACACTGCAAGATCTAATCTGGATCTGCAACTGGAAT
ATGGACAAGGACACCAAGGTGGTTACTTTTTAGGTGCAACAAGAGTCTTCTCAAGTCTG
TTGAAGAAGAATTGCATCAGCGAGGACACGTGCGACATTTAGAAGATGATGAAGGAGATG
ATGATGAATCTAAACACTCAACTCTGAAAGCAAAAATTCACCTCCTTTGCCACCAAGC
CTAAGTCTATCTTCATACCACAGGAAATGCATTCTACTGAGGATGAAAATCAAGGAACAA
TCAAGAGATGTCCCATGTCAGGGAGCCCAGCAAAGCCATCCCAAGTTCCACCTAGACCAC
CACCTCCCAGATTACCCCCACACAAACCTGTTGCCTTAGGAAATGGAATGAGCTCCTTCC
AGTTAAATGGTGAACGAGATGGCTCATTATGTCAACAACAGAATGAACATAGAGGCACAA
ACCTTTCAAGAAAAGAAAAGAAAGATGTACCAAAGCCTATTAGTAATGGTCTTCCTCCAA
CACCTAAAGTGCATATGGGTGCATGTTTTTCAAAAGTTTTTAATGGGTGTCCCTTGAAAA
TTCCTGTGCATCATCATGGATAAACCCAGATACAAGAGATCAGTACTTGATATTTGGTG
CCGAAGAAGGGATTTATACCCTCAATCTTAATGAACTTCATGAAACATCAATGGAACAGC
TATTCCTCGAAGGTGTACATGGTTGTATGTAATGAACAATTGCTTGCTATCAATATCTG
GTAAAGCTTCTCAGCTTTATTCCCATAATTTACCAGGGCTTTTTTGATTATGCAAGACAAA
TGCAAAAGTTACCTGTTGCTATTCCAGCACACAAACTCCCTGACAGAATACTGCCAAGGA
AATTTTCTGTATCAGCAAAAATCCCTGAAACCAAATGGTGCCAGAAGTGTTGTGTTGTAA
GAAATCCTTACACGGGCCATAAATACCTATGTGGAGCACTTCAGACTAGCATTGTTCTAT
TAGAATGGGTTGAACCAATGCAGAAATTTATGTTAATTAAGCACATAGATTTTCTATAC
CATGTCCACTTAGAATGTTTGAAATGCTGGTAGTTCCTGAACAGGAGTACCCTTTAGTTT
GTGTTGGTGTGAGTAGAGGTAGAGACTTCAACCAAGTGGTTCGATTTGAGACGGTCAATC
CAAATTCTACCTCTTCATGGTTTACAGAATCAGATACCCACAGACAAATGTTACTCATG
TAACCCAACTGGAGAGAGATAACCATCCTTGATGCTTGGACTGTTGTATAAAAATAGTAA
ATCTCCAAGGAAGATTAAAATCTAGCAGGAAATTGTCATCAGAACTCACCTTTGATTTCC
AGATTGAATCAATAGTGTGCCTACAAGACAGTGTGCTAGCTTTCTGGAAACATGGAATGC
AAGGTAGAAGTTTTAGATCTAATGAGGTAACACAAGAAATTTAGATAGCACAGAATTT
TCAGGCTGCTTGGATCTGACAGGGTCGTGGTTTTGGAAAGTAGGCCAACTGATAACCCCA
CAGCAAATAGCAATTTGTACATCCTGGCGGGTCATGAAAACAGTTACTGAGAATTGTTGT
GCTTTGACAGTTAACTCTAGAAAGAAAGAACTACCACTGCAACATTAATGGATGCTTG
AAGCTGTACAAAAGCTGCAGTAACCTGTCTTCAGTTACTTTGTAATTTATTGTGGCATGA
GATAAGATGGGGAAAATTTTGTTTTAAGTGGTATGGATATATTTAGCATATTGAACCACA
CAAGTGCTTAATTCATTGTTATGTAATCTTTGTACATATAGGCAGTATTTTTCTGTGAA
ACTTCATATTGCTGAAGACATACACTAAGAATTTATGTAGATAATGTACTTTTATGAGAT
GTACAAGTAAGTGTCTTATCTGTACAGATGTAAATGTTGATGAAAATGCAATTGGGGTTA
ATATTTTAAGAATTCCTTAGTATATTCTTGGGTGTGGCTATATTACAAAATGGGATGCTG
GCAATGAAACAATACATTTAACACTATTGTATTTTTATTATATGTAATTTAGTAATATGA

Fig. 9M

45/76

ATATAAATCTTGTAACCTTTTAAAATTGTAATGGAGGCTGTAATCATTTTTATAATCTTTTT
AATTTTAATGCAAGTACACTGGTGTTTATATTTGCACAAAGTATTGATATGTGATGTATT
AAGTCACAAAAGTAAGCTGTGACATTGTCTATAAGCATTGGCTCCACAAATGTATTTGG
ATTGTTTTCTATGTGAAGCAAACCAATTATAATTAACCACATGTTGTAGTAACTGGTCTT
TTTATATTTAAGCAGAATCCTGTAAGATTGCTTGTCTTTGCTTAAAAACAATACCTTTGA
ACATTTTTGAATCACAGAATAGCGGTACCATGATAGAATACTGCAATTGTGGTCAGAATT
ACAGTATGCACAAAGAATTAATTAGCATTATTAAGAGAGTCCTCACTAAACATTTTCATATG
ATCACACTGAAGAACTGTAACATTCCATAGAGTGAAGTGGTTCAAATTTCTCTTGGGAATT
TTTACTTTTGTGGCCTTATTTTATGATCCTTTTCATATTTCTTTTGACTTAGAGTATTA
ATACATGGCCAAAATAATTTAGTTACTACCTCATACAAACAATATAATGGTTACTACACA
TCACAGGAACCTTAGTTTTGGTTTAAAGTCATTTTTGATTGCTTTTTTCCAATGGAATATGT
ATATACCAGGTTTTAGCAAAATGCACACTTTTGGCTCTTTTTGGTATATGTTCTTTATAT
TTTAATGTGAGTATATACACTAAGAACAACTAAATTGTGATTTATGATCTTCATTTATT
TTAATGATAATGGTTTTAAAATATGTTCTGATTGTACATATTGTAAAATAAACATGTTT
TTT

SEQ ID NO: 19 SULU1 HUMAN

GGGAGGGTCCTTGTGGCGCCGGGCGGGGTCCTGCGTGGAGAGTGGGACGCAACGCCG
AGACCGCGAGCAGAGGCTGCGCACAGCCGGATCCGGCACTCAGCGACCGGACCCAAGGAT
CCGCCGGGGAACAAGCCACAGGAGAGCGACTCAGGAACAAGTGTGGGAGAGGAAGCGGCG
GCGGCGGCGCCGGGCCCCGGGGGTGGTGACAGCAGGTCTGAGGTTGCATCATAAATACAAA
GGACTGAAGTTATAAAAAGAGAAAAGAGAAGTTTGCTGCTAAAATGAATCTGAGCAATATG
GAATATTTTGTGCCACACACAAAAAGGTACTGAAGATTTACCCCCCAAAAAAATTGTCA
ATGAGAAATAAAGCTAACTGATATCAAAAAGCAGAGCCTGCTCTACTGGCCATCATGCGT
AAAGGGGTGCTGAAGGACCCAGAGATTGACGATCTATTCTACAAAGATGATCCTGAGGAA
CTTTTTATTGTTTTGCATGAAATTGGACATGGAAGTTTTGGAGCAGTTTATTTTGCTACA
AATGCTCACACCAATGAGGTGGTGGCAATTAAGAAGATGTCCTATAGTGGGAAGCAGACC
CATGAGAAATGGCAAGATATTCTTAAGGAAGTTAAATTTTTACGACAATTGAAGCATCCT
AATACTATTGAGTACAAAGGCTGTTACTTGAAAGAACACACTGCTTGGTTGGTGATGGAA
TATTGCTTAGGCTCAGCCTCTGATTTATTAGAAGTTCATAAAAAACCACTTCAGGAAGTG
GAGATCGCTGCCATTACTCATGGAGCCTTGCATGGACTAGCCTACCTACATTCTCATGCA
TTGATTCATAGGGATATTAAAGCAGGAAATATTCTTCTAACAGAGCCAGGTCAGGTAAAA
CTAGCTGATTTTGGATCTGCTTCAATGGCTTCTCCTGCCAACTCCTTCGTGGGCACACCT
TACTGGATGGCTCCAGAGGTGATCTTAGCTATGGATGAAGGACAGTATGATGGGAAAGTT
GATATTTGGTCACTTGGCATCACTTGTATTGAATTGGCGGAACGGAAGCCGCCCTTTTC
AACATGAATGCAATGAGTGCCTTATATCACATTGCCCAGAATGACTCCCCAACGTTACAG
TCTAATGAATGGACAGACTCCTTTAGGAGATTTGTTGATTACTGCTTGCAGAAAATACCT
CAGGAAAGGCCAACATCAGCAGAACTATTAAGGCATGACTTTGTTCGACGAGACCGGCCA

Fig. 9N

46/76

CTACGTGTCCTCATTGACCTCATAACAGAGGACAAAAGATGCAGTTCGTGAGCTAGATAAC
CTACAGTACCGAAAAATGAAAAAATACTTTTCCAAGAGACACGGAATGGACCCTTGAAT
GAGTCACAGGAGGATGAGGAAGACAGTGAACATGGAACCAGCCTGAACAGGGAAATGGAC
AGCCTGGGCAGCAACCATTCCATTCCAAGCATGTCCGTGAGCACAGGCAGCCAGAGCAGC
AGTGTGAACAGCATGCAGGAAGTCATGGACGAGAGCAGTTCCGAAC TTGTCATGATGCAC
GATGACGAAAGCACAATCAATTCCAGCTCCTCCGTGCGTGCATAAGAAAGATCATGTATTC
ACAAGGGATGAGGCGGGCCACGGCGATCCCAGGCCTGAGCCGCGGCCTACCCAGTCAGTT
CAGAGCCAGGCCCTCCACTACCGGAACAGAGAGCGCTTTGCCACGATCAAATCAGCATCT
TTGGTTACACGACAGATCCATGAGCATGAGCAGGAGAACGAGTTGCGGGAAACAGATGTCA
GGTTATAAGCGGATGCGGCGCCAGCACCAGAAGCAGCTGATCGCCCTGGAGAACAAAGCTG
AAGGCTGAGATGGACGAGCACCGCCTCAAGCTACAGAAGGAGGTGGAGACGCATGCCAAC
AACTCGTCCATCGAGCTGGAGAAGCTGGCCAAGAAGCAAGTGGCTATCATAGAAAAGGAG
GCAAAGGTAGCTGCAGCAGATGAGAAGAAGTTCCAGCAACAGATCTTGCCCCAGCAGAAG
AAAGATTTGACAACTTTCTTAGAAAGTCAGAAGAAGCAGTATAAGATTTGTAAGGAAAAA
ATAAAAGAGGAAATGAATGAGGACCATAGCACACCCAAGAAAGAGAAGCAAGAGCGGATC
TCCAAACATAAAGAGAACTTGCAGCACACACAGGCTGAAGAGGAAGCCCACCTTCTCACT
CAACAGAGACTGTACTACGACAAAAATTGTCGTTTTCTTCAAGCGGAAAATAATGATCAAG
CGGCACGAGGTGGAGCAGCAGAACATTCGGGAGGAACTAAATAAAAAGAGGACCCAGAAG
GAGATGGAGCATGCCATGCTAATCCGGCACGACGAGTCCACCCGAGAGCTAGAGTACAGG
CAGCTGCACACGTTACAGAAGCTACGCATGGATCTGATCCGTTTACAGCACCCAGACGGAA
CTGGAAAACCAGCTGGAGTACAATAAGAGGCGAGAAAGAGAACTGCACAGAAAGCATGTC
ATGGGACTTCGGCAACAGCCAAAAAACTTAAAGGCCATGGAAATGCAAATTAAAAAACAG
TTTCAGGACACTTGCAAAGTACAGACCAAACAGTATAAAGCACTCAAGAATCACCAGTTG
GAAGTTACTCCAAAGAATGAGCACAAAACAATCTTAAAGCACTGAAAGATGAGCAGACA
AGAAAACCTTGCCATTTTGGCAGAGCAGTATGAACAGAGTATAAATGAAATGATGGCCTCT
CAAGCGTTACGGCTAGATGAGGCTCAAGAAGCAGAATGCCAGGCCTTGAGGCTACAGCTC
CAGCAGGAAATGGAGCTGCTCAACGCCTACCAGAGCAAAATCAAGATGCAAACAGAGGCA
CAACATGAACGTGAGCTCAGAAAGCTAGAGCAGAGAGTGTCTCTGCGCAGAGCACACCTT
GAGCAGAAGATTGAAGAGGAGCTGGCTGCCCTTCAGAAGGAACGCAGCGAGAGAATAAAG
AACCTATTGGAAAGGCAAGAGCGAGAGATTGAAACTTTTGACATGGAGAGCCTCAGAATG
GGATTTGGGAATTTGGTTACATTAGATTTTCTAAGGAGGACTACAGATGAGATTAAATT
TTTTGCCATTTACAAAAAAGAAAAAAGAAAAACAGAAAAAATTCAGACCCTGCAA
AACCACATTCCCCATTTTAACGGGCGTTGCTCTCACTCTCTCTCTCTTACTCTTACTG
ACATCGTGTCGGACTAGTGCTGTTTATTCTTACTCCATCAGGGGCCCCCTTCTCCCCC
CGTGTCAACTTTTCAGTGCTGGCCAAAACCTGGCCGTCTCTTCTATTTCACAGTACACGTCA
CAGTATTGATGTGATTCAAAATGTTTCAGTGAAAACCTTTGGAGACAGTTTAAACAAAACC
AATAAACCAACAACAAAAAAGTGGATGTATATTGCTTTAAGCAATCACTCATTACCACC
AATCTGTGAAAGTAAAGCAAAAAATAATAATAATAATGCCAAGGGGGAGAGAGACACAA

Fig. 9 O
47/76

TATCCGCAGCCTTACACCTTAACTAGCTGCTGCATTATTTTATTTTATTTTATTTTATTTT
GTATTTATTCATCAGGAATAAAAAAACAAGTTTTATTAAAGATTGAAAATTTGATACA
TTTTACAGAACTAATTGTGATGTACATATCAGTGGTGACATATTATTACTTTTTTGGGG
ACGGGGGGTGGGTGGGTGAAGAGATCTTGTGATTTTTTAAGAACCTGCTGGCAAGAGTT
AACTTGTCTTCAGCATATTCTGATTGTATCATAATCATTTTTCTGCTGTTGCAGAGGATGT
GAATACACTTAAGGAGCTCACAGAATCCCAGTAGCACAAATTGGGCTTTGGCAAATCGTG
TATTTTGTGTATAGAAGGAATTTAAGGAGAGGTATTACTTATTTTCATATTGTATTTTAA
CTGTTTCTCTGATCAAATTTTTTTTACTTCCTCCTCCTGTTCTCCCCACCTCCCTCCTTT
TCCAGTTCAGTATTTGGAGTTCAACACTGTCTCTCAATCAGATCATCTTGATCTTTTTCT
TTATCTCCCTTCCCCTTCTAAGTCCCATTTCTTGGTCATAAATATTGCATTATTCACAC
TTTCAAACCTGTGTATTTTCTTACAATAAAAAATGATGAAAAAAAAAAAAAAAAAAAAA

SEQ ID NO: 20 SULU3 HUMAN

TATTGAATTGGCGGAACGGAAGCCTCCTTTATTTAATATGAATGCAATGAGTGCCTTATA
TCACATAGCCCAAATGAATCCCCTACACTACAGTCTAATGAATGGTCTGATTATTTTCG
CAACTTTGTAGATTCTTGCCTCCAGAAAATCCCTCAAGATCGACCTACATCAGAGGAACT
TTTAAAGCACATATTTGTTCTTCGGGAGCGCCCTGAAACCGTGTTAATAGATCTCATTCA
GAGGACAAAGGATGCAGTAAGAGAGCTGGACAATCTGCAGTATCGAAAGATGAAGAACT
CCTTTTCCAGGAGGCACATAATGGACCAGCAGTAGAAGCACAGGAAGAAGAAGAGGAACA
AGATCATGGTGTTGGCCGGACAGGAACAGTTAATAGTGTTGGAAGTAATCAATCCATTCC
CAGCATGTCCATCAGTGCCAGCAGCCAAAGCAGTAGTGTTAACAGTCTTCCAGATGTCTC
AGATGACAAGAGTGAGCTAGACATGATGGAGGGAGACCACACAGTGATGTCTAACAGTTC
TGTTATCCATTTAAAACAGAGGAAGAAAATTACAGAGAAGAGGGAGATCCTAGAACAAG
AGCATCAGATCCACAATCTCCACCCCAAGTATCTCGTCACAAATCACACTATCGTAATCG
AGAACACTTTTGCTACTATACGGACAGCATCACTGGTTACGAGGGCAAATGCAAGAACATGA
GCAGGACTCTGAGCTTAGAGAACAATGTCTGGCTATAAGCGAATGAGGCGACAACATCA
AAAGCAACTGATGACTCTGGAAAACAAGCTAAAGGCTGAGATGGATGAACATCGCCTCAG
ATTAGACAAAGATCTTGAAACTCAGCGTAACAATTTTGCTGCAGAAATGGAGAACTTAT
CAAGAAACACCAGGCTGCCATGGAGAAAGAGGCTAAAGTGATGTCCAATGAAGAGAAAAA
ATTTAGCAACATATTCAGGCCCAACAGAAGAAAGAACTGAATAGTTTTCTCGAGTCCCA
GAAAAGAGAGTATAAACTTCGAAAAGAGCAGCTTAAAGAGGAGCTAAATGAAAACCAGAG
TACCCCCAAAAAAGAAAAACAGGAGTGGCTTTCAAAGCAGAAGGAGAATATACAGCATTT
CCAAGCAGAAGAAGAAGCTAACCTTCTTCGACGTCAAAGACAATACCTAGAGCTGGAATG
CCGTCGCTTCAAGAGAAGAATGTTACTTGGGCGTCATACTTAGAGCAGGACCTTGTCAG
GGAGGAGTTAAACAAAAGACAGACTCAGAAGGACTTAGAGCATGCCATGCTACTCCGACA
GCATGAATCTATGCAAGAACTGGAGTTCGGCCACCTCAACACAATTCAGAAGATGCGCTG
TGAGTTGATCAGATTACAGCATCAAACCTGAGCTCACTAACCAGCTGGAATATAATAAGCG
AAGAGAACGAGAACTAAGACGAAAGCATGTCATGGAAGTTCGACAACAGCCTAAGAGTTT

GAAGTCTAAAGAACTCCAAATAAAAAAGCAGTTTTCAGGATACCTGCAAAATCCAAACCAG
ACAGTACAAAGCATTAAAGAAATCACCTGCTGGAGACTACACCAAAGAGTGAGCACAAAGC
TGTTCTGAAACGGCTCAAGGAGGAACAGACCCGGAAATTAGCTATCTTGGCTGAGCAGTA
TGATCACAGCATTAAATGAAATGCTCTCCACACAAGCCCTGCGTTTGGATGAAGCACAGGA
AGCAGAGTGCCAGGTTTTGAAGATGCAGCTGCAGCAGGAACTGGAGCTGTTGAATGCGTA
TCAGAGCAAAATCAAGATGCAAGCTGAGGCACAACATGATCGAGAGCTTCGCGAGCTTGA
ACAGAGGGTCTCCCTCCGGAGGGCACTCTTAGAACAAAAGATTGAAGAAGAGATGTTGGC
TTTGCAGAATGAGCGCACAGAACGAATACGAAGCCTGTTGGAACGTCAAGCCAGAGAGAT
TGAAGCTTTTGA CTCTGAAAGCATGAGACTAGGTTTTAGTAATATGGTCCTTTCTAATCT
CTCCCCTGAGGCATTTCAGCCACAGCTACCCGGGAGCTTCTGGTTGGTCACACAACCCTAC
TGGGGGTCCAGGACCTCACTGGGGTCATCCCATGGGTGGCCACCACAAGCTTGGGGCCA
TCCAATGCAAGGTGGACCCAGCCATGGGGTCACCCTTCAGGGCCAATGCAAGGGGTACC
TCGAGGTAGCAGTATGGGAGTCCGCAATAGCCCCAGGCTCTGAGGCGGACAGCTTCTGG
GGGACGGACGGAGCAGGGCATGAGCAGAAGCACGAGTGTCACTTCACAAATATCCAATGG
GTCACACATGTCTTATACATAACTTAATAATTGAGAGTGGCAATTCGCTGGAGCTGTCT
GCCAAAAGAACTGCCTACAGACATCATCACAGCAGCCTCCTCACTTGGGTACTACAGTG
TGGAAAGCTGAGTGCATATGGTATATTTTATTCATTTTTGTAAAGCGTTCTGTTTTGTGT
TACTAATTGGGATGTCATAGTACTTGGCTGCCGGGTTTGTGGTTTGGGGAAATTTTG
AAAAGTGGAGTTGATATTAATAAATAAATGTGTATGTGTGTACATATATACACACACAT
ACACATATATTATGCATGTGGTGAAAAGAATTGGCTAGATAGGGGATTTTTCTGAACACT
GCAAAAATAGAACGTAGCAAAATGGCTTCAGTTATCACTTTTGGGTGTCTGTATCCTAAG
AAGTTTCTGAAAAGATCTAAAGCCTTTTTATCCCATATCCCAAATTCTTATGAGCCACTC
ACAGCAGGCAGCATATGTTGAAATAAGTTATTACTGGTACACACCTGCATTGCCTACCA
GTGTATTTATTTGTTATTAAATTGATCTGACTTCTCAGCCTCATTTGGACTAAAAAAGA
AAGCAGAAATCCATGAACACATTGCTTCTCGGCCTTTTGGCTAAGATCAAGTGTAGAAAT
CCATGAACACTAAAGGACTTCATTGATTTTTTTCAGAGAGTAGAAAACAACCTTAGTTTTTC
TTTTTTCCTGAATGCGTCATAGGCTTGTGAGTGATTTTTGTCCATTCAATTGTGCCTTCT
TTGTATTATGATAAGATGGGGGTACTTAAGGAGATCACAAGTTGTGTGAGGATTGCATTA
ACAAACCTATGAGCCTTCAATGGGGAAGACCAGAAGGGTGAGAGGGGGCCCTGAAAGTTCA
TATGGTGGGTATGTCCCGCAGCAGAGTGAGGAGATGAAGCTTACGTGTCCTGACGTTTTG
TTGCTTATACTGTGATATCTCATCCTAGCTAAGCTCTATAATGCCCAAGACCCCAACAG
TACTTTTACTTTGTTTGTACAAAAACAAAGACATATAGCCAATACAAATCAAATGCCGGA
GGTGTGTTGATGCCATATTTGCAAATTGCCATCTATTGAAATTCTCGTCACACTACATAGA
CATAATTGTTATCTCCTTTTGGCTTATGTGATTTTTCTGTTTACAAGTAGAATAGCCAATT
ATTTAAATGTTTAGTTGCCACAGTGAACCAGGAGTCACTGAGCCAATGACTTTACCAGCT
GCTGACTAATCTTCATCACCCTGTAGATTTTGTGCTGCATGTGCAGGTCTCTATTTTTAA
TTGCTGTTTTCTGTTGCTGCAGTACTTTACAACTTCTAGTTCTGTTGAGACTTAGTGACCA
TTTGGCATCAAGTTAACATCACACAATAGGAAACACCACTTCCACAAGTCTCAAGCCTCA

Fig. 9Q

49/76

GTGCTAAAGTACTACTGAAAAGGAACTAGGAAGTTTGGCCAATT

SEQ ID NO: 21 SULU3 MURINE

GCAGGATGCCATCAACTAACAGAGCAGGCAGTCTAAAGGACCCTGAAATTGCAGAGCTCT
TCTTCAAAGAAGATCCGGAAAAGCTCTTCACAGATCTCAGAGAAATCGGCCATGGGAGCT
TTGGAGCAGTATATTTTGCACGAGATGTGCGTACTAATGAAGTGGTGGCCATCAAGAAAA
TGTCTTATAGTGGAAGCAGTCTACTGAGAAATGGCAGGATATTATTAAGGAAGTCAAGT
TTCTACAAAGAATAAAACATCCCAACAGTATAGAATACAAAGGCTGCTATTTACGTGAAC
ACACAGCATGGCTTGTAATGGAATATTGTTTAGGATCTGCTTCAGATTTATTAGAAGTTC
ATAAAAAGCCATTACAAGAAGTGGAATAGCAGCAATTACACATGGTGCTCTCCAGGGAC
TAGCTTATTTACATTCTCATACCATGATCCATAGAGATATCAAAGCAGGAAATATCCTTC
TGACAGAACCAGGCCAAGTGAAACTTGCTGACTTTGGATCTGCTTCCATGGCTTCCCCTG
CCAATTCTTTTGTGGGAACACCATATTGGATGGCCCCAGAAGTAATTTTAGCCATGGATG
AAGGACAGTATGATGGCAAAGTTGATGTATGGTCTCTTGGAATAACGTGTATTGAATTAG
CCGAGAGGAAGCCTCCTTTATTTAATATGAATGCAATGAGTGCCTTATATCACATAGCCC
AAAATGAATCCCCTACACTACAATCTAATATGAATGATTCTTGCCTCCAGAAAATCCCTC
AAGATCGCCCTACATCAGAGGAACTTTTAAAGCACATGTTTGTTCCTTCGAGAGCGCCCTG
AAACAGTGTTAATAGATCTTATTCAAAGGACAAAGGATGCAGTAAGAGAGCTGGACAATC
TGCAGTATCGAAAGATGAAGAACTCCTTTTCCAGGAGGCACATAATGGGCCAGCGGTAG
AAGCACAGGAAGAAGAGGAGGAGCAAGATCATGGTGTGGCCGAACAGGAACAGTGAATA
GTGTTGGAAGCAATCAGTCTATCCCTAGTATGTCTATCAGTGCCAGCAGTCAAAGCAGCA
GTGTTAATAGTCTTCCAGATGCATCAGATGACAAGAGTGAGCTAGACATGATGGAGGGAG
ACCATACAGTGATGTCTAACAGTTCTGTCTATCCACTTAAACCTGAGGAGGAAAATTACC
AGGAAGAAGGAGATCCTAGAACAAAGAGCATCAGACCCACAGTCTCCCCCTCAGGTGTCTC
GTCACAAGTCACATTATCGTAATAGAGAACACTTTGCAACCATACGAACAGCATCACTGG
TTACAAGACAGATGCAAGAACATGAGCAGGACTCTGAACTTAGAGAACAGATGTCTGGTT
ATAAGCGGATGAGGCGACAGCATCAAAAGCAGCTGATGACGCTGGAAAATAAACTGAAGG
CAGAGATGGACGAACATCGGCTCAGATTAGACAAAGATCTTGAAACTCAGCGTAACAATT
TCGCTGCAGAAATGGAGAACTTATTAAGAAACACCAAGCTGCTATGGAAAAAGAGGCTA
AAGTGATGGCCAATGAGGAGAAAAAATTCCAGCAACACATTCAGGCTCAACAGAAAAAAG
AACTGAATAGCTTTTTTGGAGTCTCAAAAAAGAGAATATAAACTTCGCAAAGAGCAGCTTA
AGGAGGAGCTGAATGAAAACCAGAGCACACCTAAAAAAGAAAAGCAGGAATGGCTTTCAA
AGCAGAAGGAGAATATACAGCATTTTCAGGCAGAAGAAGAAGCTAATCTTCTTCGACGTC
AAAGGCAGTATCTAGAGCTAGAATGTCGTCGCTTCAAAAGAAGAATGTTACTTGGGCGAC
ATAACTTGGAACAGGACCTTGTCAGGGAGGAGTTAAACAAAAGGCAGACTCAAAGGACT
TGGAACATGCAATGCTATTGCGACAGCATGAATCAATGCAAGAACTGGAGTTTTCGCCATC
TCAACACTATTGAGAAGATGCGCTGTGAGTTGATCAGACTGCAGCATCAAAGTGAAGCTCA
CTAACCAGCTAGAGTACAATAAGAGAAGGGAACGGGAAGTGAAGGCGAAAACATGTCATGG

Fig. 9R

50/76

AAGTTCGACAACAACCTAAGAGTCTGAAGTCTAAAGAACTCCAAATAAAAAAGCAGTTTC
AGGATACCTGCAAAATTCAAAACCAGACAGTACAAAGCATTAAGGAATCACCTACTGGAGA
CTACACCAAAGAATGAGCACAAAGCAATC

SEQ ID NO: 25 GEK2 HUMAN

CGAAGCCACAGCCCGAGCCCGAGCCCGAGCCCGAGCCGGCGCCACCGCGCCCCCGGCCAT
GGCTTTTGGCAATTTCCGCCGCATCCTGCGCCTGTCTACCTTCGAGAAGAGAAAAGTCCCG
CGAATATGAGCACGTCCGCCGCGACCTGGACCCCAACGAGGTGTGGGAGATCGTGGGCGA
GCTGGGCGACGGCGCCTTCGGCAAGGTTTACAAGGCCAAGAATAAGGAGACGGGTGCTTT
GGCTGCGGCCAAAGTCATTGAAACCAAGAGTGAGGAGGAGCTGGAGGACTACATCGTGGA
GATTGAGATCCTGGCCACCTGCGACCAACCCCTACATTGTGAAGCTCCTGGGAGCCTACTA
TCACGACGGGAAGCTGTGGATCATGATTGAGTTCTGTCCAGGGGGAGCCGTGGACGCCAT
CATGCTGGAGCTGGACAGAGGCCTCACGGAGCCCCAGATACAGGTGGTTTGCCGCCAGAT
GCTAGAAGCCCTCAACTTTCCTGCACAGCAAGAGGATCATCCACCGAGATCTGAAAGCTGG
CAACGTGCTGATGACCCTCGAGGGAGACATCAGGCTGGCTGACTTTGGTGTGTCTGCCAA
GAATCTGAAGACTCTACAGAAACGAGATTCTTTCATCGGCACGCCTTACTGGATGGCCCC
CGAGGTGGTCATGTGTGAGACCATGAAAGACACGCCCTACGACTACAAAGCCGACATCTG
GTCCCTGGGCATCACGCTGATTGAGATGGCCCAGATCGAGCCGCCACACCACGAGCTCAA
CCCCATGCGGGTCCTGCTAAAGATCGCCAAGTCGGACCCCTCCCACGCTGCTCACGCCCTC
CAAGTGCTGTAGAGTTCCGTGACTTTCCTGAAGATAGCCCTGGATAAGAACCCAGAAAC
CCGACCCAGTGCCGCGCAGCTGCTGGAGCATCCCTTCGTGAGCAGCATCACCAGTAACAA
GGCTCTGCGGGAGCTGGTGGCTGAGGCCAAGGCCGAGGTGATGGAAGAGATCGAAGACGG
CCGGGATGAGGGGGGAAGAGGAGGACGCCGTGGATGCCGCCCTCCACCCTGGAGAACCATAC
TCAGAACTCCTCTGAGGTGAGTCCGCCAAGCCTCAATGCTGACAAGCCTCTCGAGGAGTC
ACCTTCCACCCCGCTGGCACCCAGCCAGTCTCAGGACAGTGTGAATGAGCCCTGCAGCCA
GCCCTCTGGGGACAGATCCCTCCAAACCACCAGTCCCCCAGTCGTGGCCCCTGGAAATGA
GAACGGCCTGGCAGTGCCCTGTGCCCTGCGGAAGTCCCGACCCGTGTCAATGGATGCCAG
AATTCAGGTAGCCCAGGAGAAGCAAGTTGCTGAGCAGGGTGGGGACCTCAGCCCAGCAGC
CAACAGATCTCAAAAGGCCAGCCAGAGCCGGCCCAACAGCAGCGCCCTGGAGACCTTGGG
TGGGGAGAAGCTGGCCAATGGCAGCCTGGAGCCACCTGCCCAGGCAGCTCCAGGGCCTTC
CAAGAGGGACTCGGACTGCAGCAGCCTCTGCACCTCTGAGAGCATGGACTATGGTACCAA
TCTCTCCACTGACCTGTCGCTGAACAAAGAGATGGGCTCTCTGTCCATCAAGGACCCGAA
ACTGTACAAAAAACCTCAAGCGGACACGCAAATTTGTGGTGGATGGTGTGGAGGTGAG
CATCACCACTCCAAGATCATCAGCGAAGATGAGAAGAAGGATGAGGAGATGAGATTTCT
CAGGCGCCAGGAACTCCGAGAGCTTCGGCTGCTCCAGAAAGAAGAGCATCGGAACCAGAC
CCAGCTGAGTAACAAGCATGAGCTGCAGCTGGAGCAAATGCATAAACGTTTTGAACAGGA
AATCAACGCCAAGAAGAAGTTCTTTGACACGGAATTAGAGAACCTGGAGCGTCAGCAAAA
GCAGCAAGTGGAGAAGATGGAGCAAGACCATGCCGTGCGCCGCCGGGAGGAGGCCAGGCG

GATCCGCCTGGAGCAGGATCGGGACTACACCAGGTTCCAAGAGCAGCTCAAACCTGATGAA
GAAAGAGGTGAAGAACGAGGTGGAGAAGCTCCCCGACAGCAGCGGAAGGAAAGCATGAA
GCAGAAGATGGAGGAGCACACGCAGAAAAAGCAGCTTCTTGACCGGGACTTTGTAGCCAA
GCAGAAGGAGGACCTGGAGCTGGCCATGAAGAGGCTCACCCACCGACAACAGGCGGGAGAT
CTGTGACAAGGAGCGCGAGTGCCTCATGAAGAAGCAGGAGCTCCTTCGAGACCGGGAAGC
AGCCCTGTGGGAGATGGAAGAGCACCAGCTGCAGGAGAGGCAACCAGCTGGTGAAGCAGCA
GCTCAAAGACCAGTACTTCCTCCAGCGGCACGAGCTGCTGCGCAAGCATGAGAAGGAGCG
GGAGCAGATGCAGCGCTACAACCAGCGCATGATAGAGCAGCTGAAGGTGCGGCAGCAACA
GGAAAAGGCGCGGCTGCCCAAGATCCAGAGGAGTGAGGGCAAGACGCGCATGGCCATGTA
CAAGAAGAGCCTCCACATCAACGGCGGGGGCAGCGCAGCTGAGCAGCGTGAGAAGATCAA
GCAGTTCTCCCAGCAGGAGGAGAAGAGGCAGAAGTCGGAGCGGCTGCAGCAACAGCAGAA
ACACGAGAACCAGATGCGGGACATGCTGGCGCAGTGCGAGAGCAACATGAGCGAGCTGCA
GCAGCTGCAGAATGAAAAGTGCCACCTCCTGGTAGAGCACGAAACCCAGAAACTGAAGGC
CCTGGATGAGAGCCATAACCAGAACCTGAAGGAAT

SEQ ID NO: 27 PAK4 HUMAN

CGTTCCTGGGCTTCCCGCTCCGCAGGCCTGCGGAGGACTGGCCCAGCAAGGTCCCAGGTC
TTCCCTCTCCTTAGCGCCTAAGAGAGAGGGCCAGTGCGGGTGAGGAGTCGCGAGGAAGAG
GCGGAAGGCGCCGGAAGGCACCATGTTCCGCAAGAAAAAGAAGAAACGCCCTGAGATCTC
AGCGCCACAGAACTTCCAGCACCGTGTCCACACCTCCTTCGACCCCAAGAAGGCAAGTT
TGTGGGCCTCCCCCACAATGGCAGAACATCCTGGACACACTGCGGCGCCCCAAGCCCGT
GGTGGACCCTTCGCGAATCACACGGGTGCAGCTCCAGCCCATGAAGACAGTGGTGCGGGG
CAGCGCGATGCCTGTGGATGGCTACATCTCGGGGCTGCTCAACGACATCCAGAAGTTGTC
AGTCATCAGCTCCAACACCCTGCGTGGCCGCAGCCCCACCAGCCGGCGGGGCACAGTC
CCTGGGGCTGCTGGGGGATGAGCACTGGGGCCACCGACCCAGACATGTACCTCCAGAGCCC
CCAGTCTGAGCGCACTGACCCCCACGGCCTCTACCTCAGCTGCAACGGGGGCACACCAGC
AGGCCACAAGCAGATGCCGTGGCCCGAGCCACAGAGCCCACGGGTCTGCCCCAATGGGCT
GGCTGCAAAGGCACAGTCCCTGGGGCCCCGCGAGTTTCAGGGTGCTTCGCAGCGCTGTCT
GCAGCTGGGTGCCTGCCTGCAGAGCTCCCCACCAGGAGCCTCGCCCCCACGGGCACCAA
TAGGCATGGAATGAAGGCTGCCAAGCATGGCTCTGAGGAGGCCCGGCCACAGTCCTGCCT
GGTGGGCTCAGCCACAGGCAGGCCAGGTGGGGAAGGCAGCCCTAGCCCTAAGACCCGGGA
GAGCAGCCTGAAGCGCAGGCTATTCCGAAGCATGTTCTGTCCACTGCTGCCACAGCCCC
TCCAAGCAGCAGCAAGCCAGGCCCTCCACCACAGAGCAAGCCCCAACTCCTCTTTCCGACC
GCCGCAGAAAGACAACCCCCCAAGCCTGGTGGCCAAGGCCCAGTCCTTGCCCTCGGACCA
GCCGGTGGGGACCTTCAGCCCTCTGACCACTTCGGATAACAGCAGCCCCCAGAAGTCCCT
CCGCACAGCCCCGGCCACAGGCCAGCTTCCAGGCCGGTCTTCCCCAGCGGGATCCCCCG
CACCTGGCACGCCCAGATCAGCACCAAGCAACCTGTACCTGCCCCAGGACCCCCACGGTTGC
CAAGGGTGCCCTGGCTGGTGAGGACACAGGTGTTGTGACACATGAGCAGTTCAAGGCTGC

Fig. 9T
52/76

GCTCAGGATGGTGGTGGACCAAGGGTGACCCCGGCTGCTGCTGGACAGCTACGTGAAGAT
TGGCGAGGGCTCCACCGGCATCGTCTGCTTGGCCCGGGAGAAAGCACTCGGGCCGCCAGGT
GGCCGTCAAGATGATGGACCTCAGGAAGCAGCAGCGCAGGGAGCTGCTCTTCAACGAGGT
GGTGATCATGCGGGACTACCAGCACTTCAACGTGGTGGAGATGTACAAGAGCTACCTGGT
GGGCGAGGAGCTGTGGGTGCTCATGGAGTTCCTGCAGGGAGGAGCCCTCACAGACATCGT
CTCCCAAGTCAGGCTGAATGAGGAGCAGATTGCCACTGTGTGTGAGGCTGTGCTGCAGGC
CCTGGCCTACCTGCATGCTCAGGGTGTCTATCCACCGGGACATCAAGAGTGACTCCATCCT
GCTGACCCTCGATGGCAGGGTGAAGCTCTCGGACTTCGGATTCTGTGCTCAGATCAGCAA
AGACGTCCCTAAGAGGAAGTCCCTGGTGGGAACCCCTACTGGATGGCTCCTGAAGTGAT
CTCCAGGTCTTTGTATGCCACTGAGGTGGATATCTGGTCTCTGGGCATCATGGTGATTGA
GATGGTAGATGGGGAGCCACCGTACTTCAGTGACTCCCCAGTGCAAGCCATGAAGAGGCT
CCGGGACAGCCCCCACC CAAGCTGAAAACTCTCACAAGGTCTCCCCAGTGCTGCGAGA
CTTCCTGGAGCGGATGCTGGTGCGGGACCCCCAAGAGAGAGCCACAGCCCAGGAGCTCCT
AGACCACCCCTTCCTGCTGCAGACAGGGCTACCTGAGTGCCTGGTGCCCTGATCCAGCT
CTACCGAAAGCAGACCTCCACCTGCTGAGCCCACCCCAAGTATGCCTGCCACCTACGCCC
ACAGGCAGGGCACACTGGGCAGCCAGCCTGCCGGCAGGACTTGCTGCTCCTCCTCTCA
GTATTCTCTCCAAAGATTGAAATGTGAAGCCCCAGCCCCACCCTCTGCCCTTCAGCCTAC
TGGGCCAGGCCGGACCTGCCCCCTCAGTGTCTCTCCCTCCCGAGTCCCCAGATGGAGACC
CCTTTCTACAGGATGACCCCTTGATATTTGCACAGGGATATTTCTAAGAAACGCAGAGGC
CAGCGTTCCTGGCCTCTGCAGCCAACACAGTAGAAAAGGCTGCTGTGGTTTTTTAAAGGC
AGTTGTCCACTAGTGTCTTAGGCCACTGCAGAGGGCAGACTGCTGGTCTCCACAGATACC
TGCTGTTCTCAGCTCCAGCTTCAAACCTCGAGTCTCGAGAGGGCCACGGGGTGGTTTTTA
TGACCGGAATCCCGCTTCCTCCCTCACGTCTGATGTCCTGAAGGTGCAGTCCCACCTGTA
CAGCCCCCTCCCCGCCAAGAACTGTGAATGGCCTGCTCCAGGCCATGGCTGGGGGCAGGGA
GTGAGGGGACAATTTCTGAGTGAAAGAGAAAGAATGGGGTCGGTGGTGAAGGTGCTCTCA
CTTTACAGAATGGAGAGAACATCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG
TG
CCTCCAGGTCACCCACAGCCAGTTTCAGGAAGGCTGCCCCCTCTCTCCCACTAAGTTCTGG
CCTGAAGGGACCTGCTTTCTTGGCCTGGCTTCCACCTCTCCACTCCTGTGTCTACCTGGC
CAGTGGAGTGGTCCATGCTAAGTCTAACACTCCTGGGAGCTCAGGAGGCTTCTGAGCTTC
TCCTGTACTGTGCATCGTGAGGGCCAGAGACAGGAATGTAAGGATTGGCAACTGTGTTAC
CTTTCAAGTTTATCTCAATAACCAGGTCATCAGGGACCCATTGTTCTCTTCAGAACCTTA
TCTGGGAGAGAAGGCGAACCACTCCGGGTTTCCATCATGTCAAGGTACAGGCATCCAT
GTGTGCAAACCATCTGCCCCAGCTGCCTCCACAGACTGCTGTCTCCTTGTCTCCTCCTCGGC
CCTGCCCCACTTCAGGGCTGCTGTGAGATGGAATTCCAGGAAAGAACTTCAGGTGTCTGG
ACCCTTTCTATCTAGATAATATTTTTAGATTCTTCTGCTCCCTAGTGACCTACCTGGGGG
CAAAGAAATTGCAAGGACTTTTTTTTAAAGGGTCAGAGTTTTCAAACAAAAGCATCTTCC
CTAGAAATTTTTGTGAATTGTTTGCCTTGTGCCTGTTTTAAATTAAATTGAGTGTTCAA

Fig. 9U

53/76

AGCC

SEQ ID NO: 28 PAK5 HUMAN

GGCCAGTGGGGCGAAACTGGCAGCTGGCCGGCCCTTTAACACCTACCCGAGGGCTGACAC
GGACCACCCATCCCGGGGTGCCCAGGGGGAGCCTCATGACGTGGCCCTAACGGGGCCATC
AGCGGGGGGCTGGCCATCCCCCAGTCCTCCTCCTCCTCCTCCCGGCCTCCCACCCGAGC
CCGAGGTGCCCCCAGCCCTGGAGTGCTGGGACCCCCACGCCTCAGAGCCCCAGCTGGCCCC
TCCAGCCTGCACCCCCGCCGCCCTGCTGTTCTTGGGCCCCCTGGCCCCCGCTCACCACA
GCGGGAGCCACAGCGAGTATCCCATGAGCAGTTCCGGGGCTGCCCTGCAGCTGGTGGTGGA
CCCAGGCGACCCCCGCTCCTACCTGGACAACCTTCATCAAGATTGGCGAGGGCTCCACGGG
CATCGTGTGCATCGCCACCGTGCGCAGCTCGGGCAAGCTGGTGGCCGTCAAGAAGATGGA
CCTGCGCAAGCAGCAGAGGCGCGAGCTGCTCTTCAACGAGGTGGTAATCATGAGGGACTA
CCAGCACGAGAATGTGGTGGAGATGTACAACAGCTACCTGGTGGGGGACGAGCTCTGGGT
GGTCATGGAGTTCCTGGAAGGAGGCGCCCTCACCGACATCGTCACCCACACCAGGATGAA
CGAGGAGCAGATCGCGGCCGTGTGCCTTGCAGTGCTGCAGGCCCTGTCGGTGCTCCACGC
CCAGGGCGTCATCCACCGGGACATCAAGAGCGACTCGATCCTGCTGACCCATGATGGCAG
GGTGAAGCTGTCAGACTTTGGGTTCTGCGCCCAGGTGAGCAAGGAAGTGCCCCGAAGGAA
GTCGCTGGTCGGCACGCCCTACTGGATGGCCCCAGAGCTCATCTCCCGCCTTCCCTACGG
GCCAGAGGTAGACATCTGGTCGCTGGGGATAATGGTGATTGAGATGGTGGACGGAGAGCC
CCCCTACTTCAACGAGCCACCCCTCAAAGCCATGAAGATGATTCGGGACAACCTGCCACC
CCGACTGAAGAACCTGCACAAGGTGTCGCCATCCCTGAAGGGCTTCTTGGACCGCCTGCT
GGTGCGAGACCCTGCCCAGCGGGCCACGGCAGCCGAGCTGCTGAAGCACCCATTCTGGC
CAAGGCAGGGCCGCCTGCCAGCATCGTGCCCTCATGCGCCAGAACCGCACCCAGATGAGG
CCCAGCGCCCTTCCCCTCAACCAAAGAGCCCCCCCCGGGTACCCCCGCCCCACTGAGGCC
AGTAGGGGGCCAGGCCTCCCCTCCTCCCAGCCCCGGGAGATGCTCCGCGTGGCACCAACC
TCCTTGCTGGGGGTAGATGAGACCCTACTACTGAACTCCAGTTTTGATCTCGTGACTTTT
AGAAAAACACAGGGACTCGTGGGAGCAAGCGAGGCTCCCAGGACCCCCACCTCTGGGAC
AGGCCCTCCCCCATGTTCTTCTGTCTCCAGGAAGGGCAGCGGCCCTCCCATCACTGGAAG
TCTGCAGTGGGGGTGCTGGGGGTGGAGAGAACTAAGAGGTGAACATGTATGAGTGTG
TGCACGCGTGTGAGTGTGCATGTGTGTGTGTGTGCAAAGGTCCAGCCACCCCGTCCTCCA
GCCCCGAAGGGGTGTCTGGCGCCTTGCTGACACCCAGCCCCCTCTCCCCCTGAGCCATT
GTGGGGGTGATCATGAATGTCCGAAGAGTGGCCTTTTCCCGTAGCCCTGCGCCCCCTTT
CTGTGGCTGGATGGGGAGACAGGTCAGGGCCCCCACCCTCTCCAGCCCCCTGCAGCAAAT
GACTACTGCACCTGGACAGCCTCCTCTTTTCTAGAAGTCTATTTATATTGTCATTTTATA
ACACTCTAGCCCCCTGCCCTTATTGGGGGACAGATGGTCCCTGTCTGCGGGGTGGCCCTG
GCAGAACCACTGCCTGAAGAACCAGGTTCTTGCCCGGTGAGCGCAGCCCCAGCCCGCCCA
CCCCTGCCTCGAGTTAGTTTTACAATTAACATTGTCTTGTGTTTTGTGAAAAAAAAAAAA
AAAAAAAAAA

Fig. 9V
54/76

>STLK5_h

MSSFLPEGGCYELLTVIGKGFEDLMTVNLARYKPTGEYVTVRRINLEACSNEMVTLQGELHVSKLFNHPNIVPYRATFI
ADNELWVTSFMAYGSAKDLICTHFMDSGMNELAIAYILQGVLKALDYIHMGYVHRSVKASHILISVDGKVYLSGLRSNL
SMISHGQRQVRVHDFPKYSVKVLPWLSPEVLQQLQGYDAKSDIYSVGITACELANGHVPFKDPATQMLLEKLNGLTVPC
LLDTSTIPAEELTMSPSRSVANSGLSDSLTTSTPRPSNGDSPSHPHYHRTFSPHFHFVEQCLQRNPDARPSASTLLNHSF
FKQIKRRASEALPELLRPVPTITNFEQSQDHSIGIFGLVTNLEELEVDWDF

>STLK6_h

MSLLDCFCSTRTQVESLRPEKQSETSIHQYLVDEPTLSWSRPSTRASEVLCSTNVSHYELQVEIGRGFDNLTSVHLARHT
PTGTLVTIKITNLENCNEERLKALQKAVILSHFFRHPNITTYTFTVGSWLWVISPFMAYGSASQLLRTYFPEGMSETL
IRNILFAGVRGLNYLHQNCIHRSIKASHILISGDGLVTL SGLSHLSLVKHGQRHRAVYDFPQFSTSVQPWLSPELLRQ
DLHGYNVKS DIYSVGITACELASGVVPFQDMHRTQMLLQKLKPPYSPLDISIFPQSESRMKNSSQSGVDSGIGESVLVSS
GHTVNSDRLHTPSSKTFSPAFFSLVQLCLQQDPEKRPSASSLLSHVFFKQMKESQDSILSLLPPAYNKPSISLPPVLP
WTEPECDFPDEKDSYWEF

51
5/76

>STLK7_h

NRDDYELQEVIGSGATAVVQAAAYCAPKKEKVAIKRINLEKCKQTSMDPELLKEIQAMSQCHHPNIVSYTTSFVVKDELWLVM
KLSSGGSVLDIKIHIVAKGEHKS

>ZC4_h

MAGPGGWRDREVTDLGHLDPDTGIFSLDKTIGLTGYGRIYLGHEKTGAFATVKVMNARKDEEEDLRTELNLLRKYSFHK
NIVSYGAFKLSPPGQRHQLWMVMELCAAGSVTDVVRMTSNQSLKEDWIA YICREILQGLAHLHAHRV IHRDIKGNVL
LTHNAEVKLVD FGVSAQVSR TNGRRNSFIGTPYWM APEVIDCDEDPRRSYDYRSDVSWVGITAIEMAEGAPPLCNLQPLE
ALFVILRESAPT V KSSGWSRK FHFMEKCTIKNFLFRPT SANMLQHPFVRDIKNERHVVESLTRHLTGIIKKRQKKEQAR
EKKS K VSTLRQALAKRLSPKRFRAKSSWRPEKLELSDLEARRQRRRWEDIFNQHEEELRQVDKDESSDNDEVFHS

Fig. 10A

IQAEVQIEPLKPYISNPKKIEVQERSPSVPNNQDHAHVKFSSVPQRSLLLEQAQKPIDIRQRSSQNRQNWLAASGDSKH
KILAGKTQSYCLTIYISEVKKEEFQEGMNKCQGAQVGLGPEGHCIWQLGESSSEESPVTGRRSQSSPPYSTIDQKLLV
DIHVPDGFVKISPPVYLTNEWVGYNALSEIFRNDWLTAPAVIQPEEDGDYVELYDASADTDGDDDDDESNDTFEDTYD
HANGNDDLDNQVDQANDVC KDHDDNNKFVDDVNNNYEAPSCPRASYGRDGSCKQDGYDGSRGKEEAYRGYGSHTANRS
HGGSAASEDNAAIGDQEEHAANIGSERRGSEGDGKGVVRTSEESGALGLNGEENCSETDGPGLKRPASQDFFEYLQEEPG
GGNEASNAIDGAAPSAPDHESDNKDISESTQSDFSANHSSPSKSGMSADANFASAILYAGFVEVPEESPQKQSEVNV
NPLYVSPACKKPLIHMYEKEFTSEICCGSLWGVNLLGTRSNLYLMDRSGKADITKLIRRRPFRQIQVLEPLNLLITISG
HKNRLRVYHLTWLRNKILNNDPESKRQRQEMLKTEEACKAIDKLTGCEHFSVLQHEETTYIAIALKSSIHLYAWAPK'SFD
ESTAICKVFPTLDHKPVTVDLAIGSEKRLKIFFSSADGYHLIDAESSEVMSDVTLPKNPLEIIIPQNIILPDCLGIGMMLT
FNAEALSVEANEQLFKKILEMWKDIPISSIAFECTQRTTGWGQKAIIEVRSLSQSRVLESELKRRSICKLRLFLCTRGDKLFFT
STLRNHHSRVYFMTLGKLEELQSNYDV

56/76

>PAK5_h

MFGKRKRVEISAPSNFEHRVHTGFDQHEQKFTGLPRQWQSLIEESARRPKPLVDPACITSIQPGAPKTIVRGSKGAKDG
ALTLLDEFENMSVTRNSLRRDSPPPPARARQENGMPPEEATTARGGPGKAGSRGRFAGHSEAGGGSGDRRRRAGPEKRP
KSSREGSGGPQESSRDKRPLSGPDVGTQPAGLASGAKLAAGRPFNTYPRADTDHPSRGAQGEPHDVAPNGPSAGGLAIP
QSSSSSRPPTRARGAPSPGVLGPHASEPQLAPPACTPAAPAVPGPPGPRSPQREPQRVSHSEQFRAALQLVVDPGDPRSY
LDNFIKIGEGSTGIVCIATVRSSGKLVAVKKMDLRKQQRRELLFNEVIMRDYQHENVVEMYNLYLVGDELWVVMEFLEG
GALTDIVTHTRMNEEQIAAVCLAVLQALSVLHAQGVIHARDIKSDSILLTHDGRVKLSDFGFCQAQVSKEVPRRKSLVGTPY
WMAPELISRLPYGPEVDIWSLIGIMVIEMVDGEPYPFNEPPLKAMKMIRDNLPPRLKNLHKVSPSLKGFLDRLLVRDPAQR
ATAAELLKHPFLAKAGPPASIVPLMRQNRT

>GEK2_h

MAFANFRRIILRLSTFEKRKSREYEHVRRDLDPNEVWEIVGELGDGAFGKVYKAKNKETGALAAAKVIETKSEEELEDYIV
EIEILATCDHPYIVKLLGAYYHDGKLIWIMIEFCPGGAVDAIMLELDRLGLTEPQIQVVCQRMLEALNFLHSKRITIIHRDLKA

Fig. 10B

GNVLMTEGDIRLADFGVSAKNLKTLLQKRDSFIGTPYWMapevVMCETmKdTPYdYKADIWSLgITLIEMaQIEPPHHEL
NPMRVLLKIAKSDPPTLLTPSKWSVEFRDfLKIALDKNPetrPSAAQLLEHPFVSSITsNKALRELVAEAKAEVMEEIEI
GRDEGEEDAVDAASTLENHTQNSSEVSPPSLNADKPLEESPSTPLAPSQSDSVNEPCSQPSGDRSLQTTSPPVVAPGN
ENGLAVPVPLRKSrpVSMdARIQVAQEKQVAEQGGDLSPAANRSQKASQSRPNSSALETLGGEKLANGSLEPPAQAAAPGP
SKRSDCSSLCTSESMDYGTNLSTDLSLNKEMGSLSIKDPKLYKKTlKRTRKFVVDGVEVSIITTSKIISEDEKKDEEMRF
LRRQELRELRLlQKEEHRNQTQLSNKHELQLEQMhKRFEQEIINAKKKFFDTELENLERQQKQKQVEKMEQDHAVRRREEAR
RIRLEQDRDYTRFQEQlKlMKKEVKNEVEKLPRQQRKESMKQKMEEHtQKKQLLDRDFVAKQKEDLElAMKRLTTDNRRRE
ICDKERECLMKKQELLRDREAALWEMEEHQLQERHQLVKQQLKDQYFLQRHELLRKHEKEREQMQRYNQRMIEQLKVRQQ
QEKARLPKIQRSEGKTRMAMYKKS LHINGGSAAEQREKIKQFSQQEEKRQKSERLQQQKHENQMrdMLAQCESNMSEL
QQlQNEKCHLLVEHETQKLKALDESHNQNLKEWRDKLRPRKKALEEDLNQKKREQEMFFKLSEEAECNPSTPSKAAKFF
PYSSGDAS

Fig. 10C

>STLK5_h

GGCCAAAGACGGTCGGGGCTGCTTGCTAACTCCAGGAACAGGTTTAAAGTTTTTGAACCTGAAGTAGGTTCTACACAGTAGGA
ACTCATGTCTATTTCTTAAGTAAACAGAGCGAATCAGCGGTGGTCTCGGAAAGTTTCATTGTTGAGGGCTTAAAGAG
ATTTGGAACATAATTTGGAGACCAATGATGCGAGCTCAGAGTCAATAGCATCCTTCTCTAAACAGGAGGTCTAGTAGCTT
TCTGCCAGAGGGAGGTGTTACGAGCTGCTCAGTGTGATAGGCAAAAGGATTTGAGGACCTGTGATGACTGTGAATCTAGCAA
GGTACAAACCAACAGGAGAGTACGTGACTGTACGGAGGATTAAACCTAGAAAGCTTGTCCAAATGAGATGGTAACATTCTTG
CAGGGCAGCTGCATGCTCCAAACTTCAACCATCCCAATATCGTGCCATATCGAGCCACTTTTATTGCAGACAATGA
GCTGTGGGTTGTACATCATTCATGGCATACGGTTCCTGCAAAAGATCTCATCTGTACACACTTTCATGGATGGCATGAATG
AGCTGGCGATTGCTTACATCCTGCAGGGGTGCTGAAGGCCCTCGACTACATCCACCACATGGGATATGTACACAGGAGT
GTCAAAAGCCAGCCACATCCTGATCTCTGTGGATGGGAAGTCTACCTGTCTGGTTTGGCGAGCAACCTCAGCATGATAAG
CCATGGGCAGCGGAGGTGGTCCACGATTTTCCCAAGTACAGTGTCAAGTTCTGCCGTGGCTCAGCCCCGAGGTCC
TCCAGCAGAATCTCCAGGGTTATGATGCCAAGTCTGACATCTACAGTGTGGGAATCACAGCCTGTGAACCTGGCCAAACGGC
CATGTCCCCCTTTAAGGATATGCCCTGCCACCCAGATGCTGTAGAGAACTGAACGGCACAGTGCCCTGCTGCTGTTGGATAC
CAGCACCATCCCCGCTGAGGAGCTGACCATGAGCCCCCTCGCGCTCAGTGGCCAACTCTGGCCTGAGTGACAGCCTGACCA
CCAGCACCCCCGGCCCTCCAACGGTGACTCGCCCTCCACCCCTACCCAGAACCTTCTCCCCCACTTCCACCACTTT
GTGGAGCAGTGCCCTTCAGCGCAACCCGGATGCCAGGCCAGTGCCAGCACCTCCTGAACCACTCTTCTTCAAGCAGAT
CAAGCGACGTGCTCAGAGGCTTTGCCCGAATTGCTTCCTGTCACCCCTCATCAACCAATTTTGAGGGCAGCCAGTCTC
AGGACCACAGTGGAACTTTTGGCCTGGTAACAAACCTGGAAGAGCTGGAGGTGGACGATTGGGAGTTCTGAGCCTCTGCA
AACTGTGCGCATTTCCAGCCAGGATGCAGAGGCCACCCAGAGGCCCTTCTCTGAGGGCCGGCCACATTCCTCCGCCCTCCT
GGGCAGATTGGGTAGAAAGGACATTTCTCCAGGAAAGTTGACTGCTGACTGATTGGGAAAGAAATCCTGGAGAGATACT
TCACTGCTCCAAGGCTTTTGAGACACAAAGGGAATCTCAACACACAGGATCAGGAGGTCCAAAGCCGACATTCCTCAGTC
CTGTGAGCTCAGGTGACCTCTCCGCAGAAAGAGAGATGCTGCTCTGGCCCTGGGAGCTGAATTCAGGCCCAGGGTTTGG
CTCCTTAAACCCGAGGACCGCCACCTCTTCCAGTGCTTGGCAGCCAGCTCATTTCTATTAACTTTGCTCTCAGATGCTT
CAGATGCTATAGGTGAGTGAAGGGCAAGTAGTAAGCTGCCCTGCCCTTCCCTCAGACCTCTCCCTCATAAATCCAGA
GAAGGGCATTTCTGCTTTTAAAGCACAGACTAAGGCTGGAAACAGTCCATCTTATCCCTCTTCTGGCTTGGGCCCTGAC

58/76

Fig. 11A

ACCTAAGTCTTTCCACGGTTTATGTGTGCTCATTCCTTTCCACCACCAAGAAATCCATCTTAGCGCCTCCTGCCAGCTG
CCCTGGTGCTTTCTCCAGGGCCATCAGTGTCTTTGCCTAGCTTGAGGGCTTAAGTCCCTTATGCTGTGTTAGTTTCGTTGT
CAGAACAAATTAAATTTTCAGAGACGCTG

>STLK6_h

AAGGAAGATAAAACAAAAGCCTTCTTTGGAAATAGATGGATTTTGTCACTTTCTGTGAACTAAAGTGATTCAATGTCT
CTTTTGGAATTGCTTCTGCACCTTCAAGAACACAAAGTTGAATCACTCAGACCTGAAAAACAAGTCTGAAACCCAGTATCCATCA
ATACCTGGTIGATGAGCCAAACCTTTCTCTGGTCACGTCACCTCCATCCACTAGAGCCAGTGAAGTACTATGTTCACCAACGTTT
CTCACTATGAGCTCCAAGTAGAAATAGGAAGAGGATTTGACAACTTGACITTCGTCCATCTTGACCGGCATACCTCCACG
GGAACACTGGTAACATAAAATTAACAATCTGGAAACTGCAATGAAGAACGCCCTGAAAGCTTTACAGAAAGCCGTGAT
TCTATCCCACTTTTCCGGCATCCCAATATTACAACCTTATTGGACAGTTTTCACCTGTTGGCAGCTGGCTTTGGGTTATTT
CTCCATTTATGGCCATATGGTTCAGCAAGTCAACTCTTGAGGACCTATTTTCCTGAAGGAATGAGTGAACTTTAATAAGA
AACATTCTCTTTGGAGCCGTGAGGGTTGAACCTATCTGCACCAAAATGGCTGTATTACAGGAGTATTAAAGCCAGCCA
TATCCTCATTTCTGGTATGGCCTAGTGACCCCTCTCTGGCCTTTCCCATCTGCATAGTTTGTTAAGCATGGACAGAGGC
ATAGGGCTGTGTATGATTTCCACAGTTCAGCACATCAGTGCAGCCGTGGCTGAGTCCAGAACTACTGAGACAGGATTTA
CATGGGTATAATGTGAAGTCAGATATTTACAGTGTGGGATTACAGCATGTGAATTAGCCAGTGGGCAGGTGCCCTTTCCA
GGACATGCATAGAACTCAGATGCTGTTACAGAAACTGAAAGGTCTCTCTTATAGCCCATTTGGATATCAGTATTTTCCCTC
AATCAGAAATCCAGAAATGAAAAATTTCCAGTCAGGTGTAGACTCTGGGATTGGAGAAAGTGTGCTTGTCTCCAGTGGAACT
CACACAGTAAATAGTGACCGATTACACACACCATCTCTCAAAACTTTCTCTCCCTCTTCTTAGCTTGGTACAGCTCTG
TTTGCAACAAGATCCTGAGAAAGGCCATCAGCAAGCAGTTTATTGTCCCATGTTTCTTCAACAGATGAAAGAAAGAA
GCCAGGATTCAATACTTTCACTGTGCTCTCTGCTTATAACAAGCCATCAATATCATTTGCCCTCCAGTGTACCTTGGACT
GAGCCAGAAATGTGATTTTCCCTGATGAAAAAGACTCATACTGGGAATTTCTAGGGCTGCCAAATCATTTTATGTCTATATA
CTTGACACTTTCTCTGTGCTTTTCTCTGTATTTCTAGGTACAAATACAGAAATTACTTTGAAATACAGTTGGT
GCACCTGGAGAACTCTATTATTAAACCACTCTGTTCAAAAGGGGCACCAAGTTGTAGTCCCTCTGTTTCGCACAGAGTACT
ATGACAAGGAACATCAGAAATTACTAATCTAGCTAGTGTCAATTTATCTGGAAATTTTCTAAGCTGTGACTAATCTT

59/76

Fig. 11B

TTTATCTCTCAATAATAATTTTGGAGCCAGTTAATTTTTTTCAGTATTTTTTGTCTGTCCTTTGGGAATGGGCCCTCAGAGGAC
 AGTGCTTCCCAAGTACATCTTCTCCAGATCTCTGGCCCTTTTAAATGAGCTATTTGTTAAACCAACAGGCTAGTTTATCTT
 ACATCAGACCCCTTTTCTGGTAGAGGGGAAAATGTTTGTGCTTTTCCCTTTTCTTCTGTTAATACTTATGGTAAACACCTAAC
 TGAGCCCTCACTCACATTAAATGATTCACTTGAAATATATACAGAAAATTGTAATTGTCTTTTTTTTAAAAAAGGGGGCTAA
 AGTAACACTTTTCTACTTATGTAAATTATAGATCCTAAATTCACGCACCCCGTGGGAGCTCAATAAAGATTTACTGAATT

G

>STLK7_h

TCAACAGGGACGATTACGAGCTGCAGGAGGTGATCGGGAGTGGAGCAACTGCTGTAGTCCAAAGCAGCTTATTGTGCCCT
 AAAAGGAGAAAGTGGCAATCAAAACGGATAAACCTTGAGAAATGTCAAACTAGCATGGATGAACCTCTGAAAGAAATTCA
 AGCCATGAGTCAATGCCATCATCCTAATAATTGTATCTTACTACACATCTTTTGTGGTAAAGATGAGCTGTGGCTTTGTCA
 TGAAGCTGCTAAGTGGAGGTTCTGTCTGGATATTATTAAGCACATTTGTGGCAAAAGGGGAACACAAAAGT

60/76

>ZC4_h

ATGGCGGACCTGGGGCTGGAGGGACAGGGAGGTACGGATCTGGGCCACCTGCGCGGATCCAACTGGAATATTCTCACT
 AGATAAACCATTTGGCTTGGTACTTATGGCAGAACTCTATTGGGACTTCATGAGAGACTGGTGCAATTIACAGCTGTTA
 AAGTATGAACGCTCGTAAGGATGAGGAAGAGGATCTCAGGACTGAACCTCAACCTTCTGAGGAAGTACTCTTCCACAAA
 AACATTGTGTCTTCTATGGAGCAATTTTCAAGCTGAGTCCCTGTCAGCGGCACTTTGGATGGTGATGGAGTT
 ATGTGCAGCAGGTTCCGGTCACTGATGTAGTGAGAAATGACCAGTAATCAGAGTTTAAAGAAGATTGGATTGCTTATATCT
 GCCGAGAAAATCCTTCAGGGCTTAGCTCACCTTCACGCACACCCGAGTAATTCACCGGACATCAAAGTCAAGATGTGCTG
 CTGACTCATAAATGCTGAAGTAAACTGGTTGATTTTGGAGTGAGTGCCTCCAGGTGAGCAGAACTAATGGAAAGGAATAG
 TTTTCATTGGGACACCATACTGGATGGCACCTGAGGTGATTGACTGTGATGAGGACCCCAAGACGCTCCTATGATTACAGAA
 GTGATGTGTGGTCTGTGGGAATTACTGCCATTGAAATGGCTGAAGGAGCCCTCTCTGTGTAACTTCAACCTTGGAA
 GCTCTCTTCGTTATTTTGGGGGAATCTGCTCCACAGTCAAAATCCAGCGGATGGTCCCGTAAGTTCACAAATTCATGGA
 AAAGTGACGATAAAAATTTCTGTCTCTACTTCTGCAAAACATGCTTCAACACCCCAATTTGTTCGGGATATAAAA

Fig. 11C

ATGAACGACATGTTGTTGAGTCATTAAACAAGGCATCTTACTGGAATCATTAATAAAGACAGAAAGAACAGGCACGG
GAGAAAAATCAAAAGTTTCTACTCTGAGGCAAGCACTGGCAAAAAGACTATCACCAAAGAGGTTTCAGGGCAAAGTCATC
ATGGAGACCTGAAAAGCTTGAACCTCTCGGATTTAGAAAGCCCGCAGGCAAGCGCCAAACGAGATGGGAAGATATCTTTA
ATCAGCATGAGGAAGAATTGAGACAAAGTTGATAAAGACAAAGAGATGAATCATCAGACAAATGATGAAGTATTTCAATTCG
ATTGAGGCTGAAGTCCAGATAGAGCCATTGGAAGCCATACATTTCAAATCCTAAAAAATTTGAGGTTCAAGAGAGATCTCC
TTCTGTGCCCTAACAAACAGGATCATGTCACATCATGTCAAGTTCTCTTCAAGCGTTCTCTCAGCGGTCCTTTTGGAAACAAG
CTCAGAAGCCCATTTGACATCAGACAAAGGAGTTTCGCAAAATCGTCAAAATTTGGCTGGCAGCATCAGGTGATTTCAAAGCAC
AAAAATTTAGCAGGCAAAACACAGAGCTACTGTTTAAACAATTTATATTTCAAGAAGTCAAGAAAGAAATTTCAAGAAGG
AATGAATCAAAAGTGTGAGGAGCCCAAGTAGGATTAGGACCTGAAGGCCATTGTATTTGGCAATTTGGGTGAATCTTCTT
CTGAGGAAGAAAGTCTGTGACTGGAAGGAGGTCTCAGTCAATCACCACTTATTTCTACTATTGATCAGAAAGTTGCTGGTT
GACATCCATGTTCCAGATGGATTTAAAGTAGGAAAAATATCACCCCTGTATACCTTGACAAACGAATGGGTAGGCTATAA
TGCACTCTCTGAAATCTTCCGGAATGATTGGTTAACTCCGGCACCTGTCAATTCAGCCACCTGAAGAGGATGGTGATTATG
TTGAACCTCTATGATGCCAGTGTGATACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
CATGCCAATGGCAATGATGACITGGATAACCAAGGTTGATCAGGCTAATGATGTTTGTAAAGACCATGATGATGACAAACA
TAAGTTTGTGATGATGATAATAATAATTATATGAGGCGCTAGTTGTCCAAAGGCAAGCTATGGCAGAGATGGAAAGCT
GCAAGCAAGATGGTTATGATGGAAGTCTGGAAAGAGGAGCCCTACAGAGGCTATGGAAAGCCATACAGCCCAATAGAAAGC
CATGGAGGAAGTGACCCAGTGAGGACAAATGCAGCCATTGGAGATCAGGAAGACATGCAGCCCAATATAGGCAGTGAAAG
AAGAGGCAGTGAGGATGAGGAGTCTGTTCCGAACCAAGTGAAGAGAGTGAGGCCCTTGGACTCAATGGAGAG
AAAATTGCTCAGAGACAGATGTTCCAGGATTGAAGAGACCTGCGTCTCAGGACTTTGAATATCTACAGGAGGAGCCAGGT
GGTGGAAATGAGGCTCAAAATGCCATTGACTCAGGTGCTGCCACCTGATCATGAGAGTGACAAATAAGGACAT
ATCAGAATCATCAACAAATCAGATTTTCTGCCAATCACTCATCTCCTTCCAAAGGTTCTGGGATGTCTGCTGATGCTA
ACTTTGCCAGTGCCCATCTTATACGCTGGATTCTGTAAGATACCTGAGGAATCACCTAAGCAACCCCTCTGAAGTCAATGTT
AACCACCTCTATGCTCTCTGCAATGTAAAAAACCACTAATCCACATGTATGAAAAAGGAGTTCACTTCTGAGATCTGCTG
TGGTCTTTTGTGGGAGTCAATTTGCTGTTGGGAACCCGATCTAATCTATATCTGATGGACAGAGTGGAAAGGCTGACA
TTACTAAACTTATAAGGCGAAGACCATTTCCGCCAGATTCAAGTCTTAGAGCCCACTCAATTTGCTGATTACCATCTCAGGT

91/76

Fig. 11D

>PAK5_h

CCGGAGTGTC CGCGGTGGTGGCGGTGCAAGAGAGCTGAAGGAGGCGCGGAGGGCGCGGAGTTCCAGGCCGAGCAGTTAGGC
 CCGGAGCGACTGCGGCGCGAGCCGATGAGTAACCCGAAGCCCTAGAGGAGTGGTCACCTGCCTGAGGGCACTTCTGTCTC
 CCCACCAAGCATCAGACCAGGCCGACCGAGTCCCCGGCACCATGTTTGGGAAGAGGAAGCGGGTGGAGATCTCCGCGCG
 CGTCCAACTTCGAGCACCGCGTGCCACACGGGCTTCGACCAGCACGAGCAGAAATTACGGGGCTGCCCCGCTAGTGGCAG
 AGCTGATCGAGGAGTCGGCTCGCCGGCCCCAAGCCCCTCGTCGACCCCGCTGCATCACCTCCATCCAGCCCCGGGCCCC
 CAAGACCATCGTGGCGGGCAGCAAGGTGCCAAAGATGGGGCCCCACGCTGCTGGAACGAGTTTGAGAAACATGTCGG
 TGACACGCTCCAACCTCCCTGCGGAGAGACAGCCCGCCGCGCCGCTGCCCGCAGGAAATGGGATGCCAGAGGAG
 CCGGCCACCA CGGCCAGAGGGGGCCCCAGGGAAAGGCAGCCGAGGCCGCTCGCCGGTCA CAGCAGCGCGGTGGCGG
 CAGTGGTGACAGGCGACGGGCGGGGCCAGAGAAGAGGCCCAAGTCTTCCAGGGAGGGCTCAGGGGGTCCCCAGGAGTCTCT
 CCGGGGACAAACGCCCTCTCCGGGCTGATGTCGGCACCCCCAGCTGCTGGTCTGGCCAGTGGGGCGAAACTGGCA
 GCTGGCGGCCCTTAACACCTACCCGAGGGCTGACACGGACCAACCATCCCCGGGGTGCCCAAGGGGAGCCTCATGACGT
 GGGCCCCTAACGGGCCCATCAGCGGGGGGCGCTGGCCATCCCCCAGTCTCTCTCTCCCGGGCTTCCCAACCCGAGCCCC

Fig. 11E

GAGGTGCCCCAGCCCTGGAGTGTCTGGGACCCACGCCTCAGAGCCCCAGCTGGCCCCCTCCAGCCCTGCACCCCCCGCCGCC
CCTGCTGTTCCCTGGGCCCCCTGGCCCCCTCACCACAGCGGGAGCCACAGCGAGTATCCCATGAGCAGTTCCGGGCTGC
CCTGCAGCTGGTGGACCCAGCGACCCCGCTCCTACCTGGACAACCTTCATCAAGATTGGCGAGGGCTCCACGGGCA
TCGTGTGCATCGCCACCGTGCGCAGCTCGGGCAAGCTGGTGGCCGTCAGAAGATGGACCTGCGCAAGCAGCAGAGGGCGC
GAGCTGCTCTTCAACGAGGTGGTAATCATGAGGGACTACCAAGCAGAGATGTGGTGAGATGTACAACAGCTACCTGGT
GGGGACGAGCTCTGGGTGGTCAATGGAGTTCCTGGAAAGGAGCGCCCTCACCGACATCGTCAACCCACACAGGATGAACG
AGGAGCAGATCGCGCGCTGTGCCCTTGCAAGTGTGAGGCCCTGTGCGTCTCCACGCCAGGGCGTCAATCCACCGGGAC
ATCAAGAGCGACTCGATCCTGCTGACCCCATGATGGCAGGGTGAAGCTGTCAAGACTTTGGGTTCTGGGCCCAGGTGAGCAA
GGAAGTGCCCCGAAAGGAGTCTGGTCGGCACGCCCTACTGGATGGCCCCAGAGCTCATCTCCCGCTTCCCTACGGGC
CAGAGGTAGACATCTGGTCGCTGGGGATAATGGTGAATGAGATGGTGGACGGAGAGCCCCCTACTTCAACGAGCCACCC
CTCAAAGCCATGAAGATGATTCTGGGACAACCTGCCACCCCGACTGAAGAACCTGCACAAAGGTGTGCGCCATCCCTGAAGGG
CTTCTCTGGACCGCTGCTGGTGCAGACCCCTGCCAGCGGGCCACCGCAGCGGCTGCTGAAGCACCCATTCCTGGCCA
AGGCAGGGCGCTGCCAGCATCGTGCCTCATGCGCCAGAACCCGACACAGATGAGGCCCCAGCGCCCTTCCCTCAACC
AAAGAGCCCCCGGGTCAACCCCGCCACTGAGGCCAGTAGGGGCCAGGCCCTCCCACTCTCCAGCCCCGGGAGATG
CTCCGCTGGCACCCCTCTTGTCTGGGGTAGATGAGACCTACTAGAACCTCCAGTTTGTATCTCGTGACTTTTAG
AAAACACAGGGACTCGTGGAGCAAGCGAGGCTCCAGGACCCCACTCTGGGACAGGCCCTCCCACTGTTCTCT
GTCTCCAGGAAGGCGAGCGCCCTCCCATCACTGGAAGTCTGCAGTGGGGTCTGGGGTGGAGAGAACACTAAGAGG
TGAACATGTATGAGTGTGTGCACGCGTGTGATGTGTGTGTGTGCAAGGTCCAGCCACCCGTCCTCCAGC
CCGCAAGGGGTGTCTGGCGCTTGCCCTGACACCCAGCCCCCTCTCCCTGAGCCATTGTGGGGTCCGATCATGATGTC
CGAAGAGTGGCCCTTTCCCGTAGCCCTGCGCCCCCTTTCTGTGGCTGGATGGGGAGACAGGTCAAGGCCCCCACTCT
CCAGCCCCCTGCAGCAAATGACTACTGCACCTGGACAGCCCTCCTCTTTCTAGAGTCTATTATATTGTCAATTTATAC
ACTCTAGCCCCCTGCCCCCTATTGGGGGACAGATGGTCCCTGTCCCTGGGGGTGGCCCCCTGGCAGAACCACTGCCCTGAAGAAC
CAGGTTCTCTGCCCCGTCAGCGCAGCCCCAGCCCCGCCCCCTGCTCGAGTTAGTTTACAATTAAACATTGTCTTGT
TTTGTG

63/76

Fig. 11F

>GEK2_h

CGAAGCCACAGCCCGAGCCCGAGCCCGAGCCCGGCGCCACCGCGCCCCCGGCCATGGCTTTTGCCAAATTTCCGCC
GCATCCTGCGCCTGTCTACCTTCGAGAAAGAGAAAGTCCCGGAAATATGAGCACGTCCGCGGACCTGGACCCCAACGAG
GTGTGGGAGATCGTGGCGGAGCTGGCGGACCGCGCCTTCGGCAAGGTTTACAAGGCCAAGAAATAAGGAGACGGGTGCTTT
GGCTGGGGCCAAAGTCATTGAACCAAGAGTGAGGAGGAGCTGGAGGACTACATCGTGGAGATTGAGATCCTGGCCACCT
GGGACCAACCCCTACATTGTGAAGCTCCTGGGAGCCTACTATCACGACGGGAAGCTGTGGATCATGATTGAGTTCTGTCCA
GGGGAGCCGTGGACGCCATCATGCTGGAGCTGGACAGAGGCCCTCACGGAGCCCCAGATACAGGTGGTTTGCCGCCAGAT
GCTAGAAGCCCTCAACTTCCTGCACAGCAAGAGGATCATCCACCGAGATCTGAAGCTGGCAACGTGCTGATGACCCCTCG
AGGGAGACATCAGGCTGGCTGACTTTGGTGTCTGTGCCAAGAACTCTGAAGACTCTACAGAAACGAGATTCCITTCATCGGC
ACGCCTTACTGGATGGCCCCGAGGTGGTCAATGTGTGAGACCATGAAGACACGCCCTACGACTACAAGCCGACATCTG
GTCCCTGGGCATCACGCTGATTGAGATGGCCCCAGATCGAGCCGCCACACGAGCTCAACCCCATGCGGGTCCCTGCTAA
AGATCGCCCAAGTCGGACCCCTCCACGCTGCTCACGCCCTCCAAAGTGTCTGTAGAGTTCCGTGACTTCCGTGAAGATAGCC
CTGGATAAGAACCCAGAAACCCGACCCAGTGCAGCCAGCTGCTGGAGCATCCCTTCGTGAGCAGCATCACCAAGTAACAA
GGCTCTGCGGGAGCTGGTGGCTGAGGCCAAGGCCGAGGTGATGGAAAGAGATCGAAGACGGCCGGGATGAGGGGGAAAGAGG
AGGACGCCGTGGATGCCGCCCTCCACCCCTGGAGAACCATACTCAGAACTCCTCTGAGGTGAGTCCGCCCAAGCCTCAATGCT
GACAAAGCCTCTCGAGGAGTCACTTCCACCCCGCTGGCACCCAGCCAGTCTCAGGACAGTGTGAATGAGCCCTGCAGCCA
GCCCTCTGGGACAGATCCCTCCAAACCAACAGTCCCGCAGTCCCGGCTGGTGGCCCTGGAAATGAGAACGGCCTGGCAGTGCCTG
TGCCCTTGCGGAAGTCCCGACCCGTGTCAATGGATGCCAGAAATTCAGGTAGCCAGGAGAACAGTTGCTGAGCAGGGT
GGGGACCTCAGCCAGCAGCCAAACAGATCTCAAAGGCCAGCCAGAGCCGGCCCAACAGCAGCGCCCTGGAGACCTTGGG
TGGGGAGAAAGCTGGCCAAATGGCAGCCTGGAGCCACCTGCCCCAGGCAGCTCCAGGGCCTTCCAAGAGGGACTCGGACTGCA
GCAGCCTCTGCACCTCTGAGAGCATGGACTATGGTACCAATCTCTCCACTGACCTGTGCTGAACAAAGAGATGGGCTCT
CTGTCCATCAAGGACCCGAAACTGTACAAAAAAACCCCTCAAGCGGACACGCCAAATTTGTGGTGGATGGTGGAGGTGAG
CATCACCACTCCAAGATCATCAGCGAAGATGAGAAAGGATGAGGAGATGAGATTTCTCAGGCGCCAGGAACTCCGAG
AGCTTCGGCTGCTCCAGAAAGAGAGCATCGGAACCCAGACCCAGCTGAGTAAACAAGCATGAGCTGCAGCTGGAGCAAAATG
CATAACGTTTTGAACAGGAAATCAACGCCCAAGAGAAAGTTCTTTGACACGGGAATTAGAGAACCTGGAGCGTCAGCAAAA

04/76

Fig. 11G

GCAGCAAGTGGAGAAGATGGAGCAAGACCATGCCGTGCGCCGCGGAGGAGGCCAGGGCGGATCCGCCCTGGAGCAGGATC
GGGACTACACCAAGGTTCCAAGAGCAGCTCAAACTGATGAAGAAAGAGGTGAAGAACGAGTGGAGAAAGCTCCCCGACAG
CAGCGGAAGGAAGCATGAAGCAGAAAGATGGAGGACACACGAGAAAGCAGCTTCTTGACCCGGGACTTTGTAGCCAA
GCAGAAAGGAGGACCTGGAGCTGGCCATGAAGAGGCTCACCAACGACAAACAGGCGGGAGATCTGTGACAAAGGAGCGCGAGT
GCCTCATGAAGAACGAGGAGCTCCCTTCGAGACCGGGAAGCAGCCCTGTGGGAGATGGAAAGACACAGCTGCAGGAGAGG
CACCAAGCTGGTGAAGCAGCAGCTCAAAGACCAGTACTTCCTCCAGCGGCACGAGCTGCTGCGCAAGCATGAGAAGGAGCG
GGAGCAGATGCAGCGCTACAACAGCGCATGATAGAGCAGCTGAAGTGCAGGAGCAACAGGAAAGGCGCGGCTGCCCA
AGATCCAGAGGAGTGAGGGCAAGACGCGCATGGCCATGTACAAGAAAGAGCCTCCACATCAACGGCGGGGCGAGCGCA'GCT
GAGCAGCGTGAGAAGATCAAGCAGTTCTCCAGCAGGAGGAGAGAGGCGGCTCGGAGCGGCTGCAGCAACAGCAGAA
ACACGAGAACCCAGATGCCGGACATGCTGCCGAGTGCGGAGCAACATGAGCGAGCTGCAGCAGCTGCAGAAATGAAAAGT
GCCACCTCCTGCTAGACACGAAACCCAGAACTGAAGGCCCTGGATGAGAGCCATAACCAAGACCTGAAGGAATGGCGG
GGACAAGCTTCGGGCCGCGCAAGAGGCTCTGGAAAGAGGATCTGAACCAAGAAAGCGGGAGCAGGAGATGTTCTTCAAGCT
GAGCGAGGAGGCGGAGTGCCCCAAACCCCTCCACCCCCAAGCAAGGCCCAAGTTCTTCCCTACAGCTCTGGGGATGCTT
CC

Fig. 11H

Fig. 12A

SPAK_h SVS 547

Fig. 12B

PAK1_h	U51120	MSNNGLDIQDKPPAPPMRNTSTMIGAGSKDAGTLNHGSKPLPPNPEEKKKKDRFYRSILP	60
PAK4_h		-----	0
PAK5_h		-----	0
PAK1_h	U51120	GDKTNKKKEKERPEISLPSDFEHTIHVGFDVAVT-GEFTGMPPEQWARLLQTTSNITKIS	115
PAK4_h		---MFRKKKKRRPEISAPQNFQHRVHTSFDPKEGKFFVGLPPQWQNILD-TLRRPKPVVDP	56
PAK5_h		---MF-GKRKKRVEISAPSNFEHRVHTGFDQHEQKFTGLPRQWQSLIEESARRPKPLVDP	56
PAK1_h	U51120	-----	115
PAK4_h		SRITRVQLQPMKTVVRGSAAMPVDGYTSGLLNDITQKLSVISNTLRGRSPTSRRRAQSLGL	116
PAK5_h		ACITSIQPGAPKTIIVRGSKGAKDGAITLLDDEFENMSVTRSNGLRRDSPPPARAR	112
PAK1_h	U51120	-----	115
PAK4_h		LGDEHWATDPDMYLQSPQSERTDPHGLYLSGNGTTPAGHKQMPWPEPQSPRVLPNGLIAAK	176
PAK5_h		-----QENGMPDEEPATTIARGGPGK	131
PAK1_h	U51120	-----	127
PAK4_h		AQSLGPAEFQGAQRCLQLGACLQSSPPGASPPPTGTNRHGMKAACHGSEEARPQSCLVGS	236
PAK5_h		AGSRGR-----FAGHS EAGGSGDRRRAAGPEKRPKSSREFGSGGPQESSRDKRP-----LSGDP	183
PAK1_h	U51120	LEFY-NSKKTSNSQKYMISFTDKS-----AEDYNSSNALNVKA-----VSETPAVPPVS	174
PAK4_h		ATGRPGGEGSPSPKTRSSSLKRLFRSMFLSTAATAPSSSKPKGPPPPQSKPNSSFRPPQK	296
PAK5_h		DVGTPOPAGLASGAKLAAG-----RPFNTYPRADTDHPSTRGAQGEPHDVA PNGP-----	232


Fig. 13A

PAK1_h U51120	E	E	D	E	D	D	D	D	D	A	T	P	P	P	V	I	A	P	R	P	E	H	T	K	S	V	T	R	S	---	V	I	E	L	P	V	T	P	T	R	D	V	A	T	S	P	I	S	P	T	E	N	N	T	I	T	230				
PAK4_h	D	N	P	P	S	L	V	A	K	A	Q	S	L	P	S	D	Q	P	V	G	T	F	S	P	L	T	T	S	D	T	S	S	P	Q	K	S	L	R	T	A	P	A	T	G	Q	L	P	G	R	S	S	P	A	G	S	P	R	T	W	H	356
PAK5_h	---	---	---	---	---	---	---	---	---	---	S	A	G	G	L	A	I	P	O	S	S	S	S	S	S	S	S	S	S	S	S	R	P	T	R	A	R	G	A	P	S	P	G	V	L	---	---	---	---	G	P	H	A	S	E	268					
PAK1_h U51120	P	---	---	---	---	---	---	---	---	---	P	D	A	L	T	L	N	T	E	K	Q	K	K	K	P	K	M	S	D	E	E	I	L	E	K	L	R	S	I	V	S	V	G	D	P	K	K	K	Y	T	R	F	E	K	I	276					
PAK4_h	A	Q	I	S	T	S	N	L	Y	L	P	Q	D	P	T	V	A	K	G	A	---	---	L	A	G	E	D	T	G	V	V	T	H	E	Q	F	K	A	A	L	R	M	V	V	D	Q	G	D	P	R	L	L	D	S	Y	V	K	I	413		
PAK5_h	P	Q	L	A	P	P	A	-	G	T	P	A	A	P	A	V	P	G	P	R	S	P	Q	R	E	P	Q	R	V	S	H	E	Q	F	R	A	A	L	Q	L	V	V	D	P	G	D	P	R	S	Y	L	D	N	F	I	K	I	327			
PAK1_h U51120	G	Q	G	A	S	G	T	V	Y	T	A	M	D	V	A	T	G	Q	E	V	A	I	K	Q	M	N	L	Q	Q	Q	P	K	K	E	L	I	T	N	E	I	L	V	M	R	E	N	K	N	P	N	I	V	N	Y	L	D	S	Y	L	V	336
PAK4_h	G	E	G	S	T	G	I	V	C	L	A	R	E	K	H	S	G	R	Q	V	A	V	K	M	M	D	L	R	K	Q	Q	R	R	E	L	L	F	N	E	V	V	I	M	R	D	Y	Q	H	E	N	V	V	E	M	Y	K	S	Y	L	V	473
PAK5_h	G	E	G	S	T	G	I	V	C	I	A	T	V	R	S	S	G	K	L	V	A	V	K	K	M	D	L	R	K	Q	Q	R	R	E	L	L	F	N	E	V	V	I	M	R	D	Y	Q	H	E	N	V	V	E	M	Y	N	S	Y	L	V	387
PAK1_h U51120	G	D	E	L	W	V	V	M	E	Y	L	A	G	G	S	L	T	D	V	V	T	E	I	C	M	D	E	G	Q	I	A	A	V	C	R	E	C	L	Q	A	L	E	S	L	H	S	N	Q	V	I	H	R	D	I	K	S	D	N	I	L	396
PAK4_h	G	E	E	L	W	V	L	M	E	F	L	Q	G	A	L	T	D	I	V	S	Q	V	R	L	N	E	E	Q	I	A	T	V	C	E	A	V	L	Q	A	L	A	Y	L	H	A	Q	G	V	I	H	R	D	I	K	S	D	S	I	L	533	
PAK5_h	G	D	E	L	W	V	V	M	E	F	L	E	G	G	A	L	T	D	I	V	T	H	T	R	M	N	E	E	Q	I	A	A	V	C	L	A	V	L	Q	A	L	S	V	L	H	A	Q	G	V	I	H	R	D	I	K	S	D	S	I	L	447
PAK1_h U51120	L	G	M	D	G	S	V	K	L	T	D	F	G	F	C	A	Q	I	T	P	E	Q	S	K	R	S	T	M	V	G	T	P	Y	W	M	A	P	E	V	V	T	R	K	A	Y	G	P	K	V	D	I	W	S	L	G	I	M	A	I	E	456
PAK4_h	L	T	L	D	G	R	V	K	L	S	D	F	G	F	C	A	Q	I	S	K	D	V	P	K	R	K	S	L	V	G	T	P	Y	W	M	A	P	E	V	I	S	R	S	L	Y	A	T	E	V	D	I	W	S	L	G	I	M	V	I	E	593
PAK5_h	L	T	H	D	G	R	V	K	L	S	D	F	G	F	C	A	Q	V	S	K	E	V	P	R	R	K	S	L	V	G	T	P	Y	W	M	A	P	E	L	I	S	R	L	P	Y	G	P	E	V	D	I	W	S	L	G	I	M	V	I	E	507
PAK1_h U51120	M	I	E	G	E	P	P	Y	L	N	E	N	P	L	R	A	L	Y	L	I	A	T	N	G	T	P	E	L	Q	N	P	E	K	L	S	A	I	F	R	D	F	L	N	R	C	L	E	M	D	V	E	K	R	G	S	A	K	E	L	L	516
PAK4_h	M	V	D	G	E	P	P	Y	F	S	D	S	P	V	Q	A	M	K	R	L	R	D	S	P	P	K	L	K	N	S	H	K	V	S	P	V	L	R	D	F	L	E	R	M	L	V	R	D	P	Q	E	R	A	T	A	Q	E	L	L	653	
PAK5_h	M	V	D	G	E	P	P	Y	F	N	E	P	L	K	A	M	K	M	I	R	D	N	L	P	P	R	L	K	N	L	H	K	V	S	P	S	L	K	G	F	L	D	R	L	L	V	R	D	P	A	Q	R	A	T	A	A	E	L	L	567	

Fig. 13B

545
 681
 591

PAK1_h	U51120	Q	H	Q	F	L	K	I	A	K	P	L	S	L	T	P	L	I	A	A	K	E	A	T	K	N	N	H
PAK4_h		D	H	P	F	L	I	Q	T	G	L	P	E	C	L	V	P	L	I	Q	L	Y	R	K	Q	T	S	T
PAK5_h		K	H	P	F	L	I	A	K	A	G	P	P	A	S	I	V	P	L	M	R	Q	N	R	T	R		

 RESIDUES THAT MATCH THE CONSENSUS NAMED CONSENSUS #1 EXACTLY.


 BOX RESIDUES THAT MATCH THE CONSENSUS EXACTLY.

Fig. 13C

ZC4_h.pro	MAGPGGWRDREVTDLGHLPDPTGIFSLDKTIIGLTYGRIYGLHEKGTGAF	50
ZC1_h.pro	MANDSPAKSLVDIDLSSLRDPAGIEELVEVVGNGTYGQVYKGRHVKTGQL	50
ZC4_h.pro	TAVKVMNARKDEEEDLRTLENLRLKYSFHKNIVSFYGAFFKLSPPGQRHQ	100
ZC1_h.pro	AAIKVMDVTEDEEEEIKLEINMLKKYSHHRNIAITYGAFTKKSPPGHDDQ	100
ZC4_h.pro	LWMVMELCAGSVTDVVRMTSNOSLKEDWIAIYICREILQGLAHLHAHRVI	150
ZC1_h.pro	LWLVMEFCGAGSITDLVKNTKGNTLKEDWIAIYSREILRGLAHLHIHVI	150
ZC4_h.pro	HRDIKGQNVLLTHNAEVKLVDFGVSAQVSRITNGRRNSFIGTPYWMapevi	200
ZC1_h.pro	HRDIKGQNVLLTEINAevklvdfgvsaqlDRTVGRRTTEIGTPYWMapevi	200
ZC4_h.pro	DCDEDPRRSYDYSRVSVSGITAIEMAEgapPLCNLQPLEALFVILRESA	250
ZC1_h.pro	ACDENPDATYDYSRDLWSGIGITAIEMAEgapPLCDMHPMRALEFIIPRNPP	250
ZC4_h.pro	PTVKSSGWSRKFFHNFMEKCTIKNFLEFRPTSANMLQHPFVRDIKNERHVVE	300
ZC1_h.pro	PRLKSKKWSSKKFFSEIEGCLVKNYMQRPSTEQLKHPEIRDPNERQVRI	300
ZC4_h.pro	SLTRHLTGIKKR-----QKKEQAREKKS	324
ZC1_h.pro	QLKDHIDRTRKRRGEKDETEYEYSGSEEEEEVEPEGEPESSIVNVPGES	350
ZC4_h.pro	KVSTLRQALAKRLSPKRRFRRAKSSWRPEKLELSDLEARRQRRQRWEDIFN	374
ZC1_h.pro	TLRDFLRLQQENKERSEALRRQQLLQEQQLREQEEYKRQLLAERQKRIE	400
ZC4_h.pro	QHEEELRQVDKDKEDSSDNDDEVFHSIOAEVQTEPLKPYISNPKKIEVQE	424
ZC1_h.pro	QQKEQRRRLEEQQRREREARRQREQEREQRRREQEEKRRRLEEELERRRKEEEE	450

Fig. 14A

ZC4_h.pro	RSPVPPNNQDHAAHHVVFSSVPQRSLLLEQAQKPIDIRQSSQNRRQNWLA	474
ZC1_h.pro	RRRAEEKRRVEREREQEYIRRQLEEEQRHLEVLQQQLLQEQAMLLLECRWRE	500
ZC4_h.pro	SGDSKHKILAGKTSYCLTIYISEVKKKEEFQEGMNOQKCGAQVGLGPEGH	524
ZC1_h.pro	MEEHRQAERLQRQLQEQAYLLSLQHDHRRPHPHQHSQQPPPPQQERSKPS	550
ZC4_h.pro	CIWQLGESSSEEEESPVTGRRSQSSPPYSTIIDQKLLVDIHVPDGFVKGIS	574
ZC1_h.pro	FHAPEPKAHYEPADRAREVEDRFRKTNHSSPEAQSKQTGRVLEPPVP	600
ZC4_h.pro	PPVYLTNEWVGYNALSEIFRNDWLTTPAPVIOPPPEEDGDYVELYDASADTD	624
ZC1_h.pro	ESFSNGNSESVHPALLQRPAPQVPVRTTSRSPVLSRRD	650
ZC4_h.pro	GDDDESNDTFEDTYDHANGNDLNDQVDDQANDVCKDHDNDNNKFVDDVN	674
ZC1_h.pro	AGQRNSTSIEPRLLWERVEKLVPRPGSSSSGSSNSGSPGSHPGSQSGS	700
ZC4_h.pro	NNYYEAPSCPRASYGRDGSCKQDGYDGSRGKEEAYRGYGSHTANRSHGGS	724
ZC1_h.pro	GERFRVRSSSKSEGPSQRLENAAVKKPEDKKEVFRPLKPADLTALAKELR	750
ZC4_h.pro	AASEDNAAIGDQEEHAANIGSERRGSEGGGKGVVRTSEESGALGLNGEE	774
ZC1_h.pro	AVEDVRPPHKVTDYSSSSEESGTTDEEDDVEQEGADESTSGPEDTRAAS	800
ZC4_h.pro	NCSETDGPGLKRRPASQDFEYVLOEEPPGGGNEASNAIDSGAAP	824
ZC1_h.pro	SLNLSNGETESVKTMIVHDDVESEPIAMTPSKEGTLIVRRTQ	850
ZC4_h.pro	KDISSESTOSDIFSANHSSPSKSGSGMSADANFASAILYAGFVEVPEE	874
ZC1_h.pro	KSSSFTFPFIDPRLLQISPSGTTVTTSVVGE	898

Fig. 14B

ZC4_h.pro	PSEVNVNPLYVSPACKKPLIHMYEKEFTSEICCGSLWGVNLLLGTRSNLY	924
ZC1_h.pro	GSVNVNPTNTRPIQSPTPEIRKRYKKRFFNSEILCAALWGVNLLVGTESGLM	948
ZC4_h.pro	LMDRSGKADITKLIRRRPFRQIQVLEPLNLLITISGHNRLRVYHLTWLR	974
ZC1_h.pro	LLDRSGQGKVPYPLINRRRFQQMDVLEGLNVLVLTISGKKDKILRVYVYLSWLR	998
ZC4_h.pro	NKILNNDPESKRRQE-EMLKTEEACKAIDKLTIGCEHFSVLQHEETIYIAI	1023
ZC1_h.pro	NKILHNDPEVEKKQGT-----TVGDLEGCVHYKVVKYERIKFLVI	1039
ZC4_h.pro	ALKSSIHLAYAWPKSFDESTAIKVFPITLDHKPVTVDLAIGSEKRLKIFFS	1073
ZC1_h.pro	ALKSSVEVYAWAPKPYHKFMAFKSFGELVHKPLLVDLTVEEGQRLKVIYG	1089
ZC4_h.pro	SADGYHLIDAESVMSDVTLPKNPLEIIPQNIILPDCLGIGMMLTFNAI	1123
ZC1_h.pro	SCAGFHAVDVDSGSVYDIYLPITHIQCSIKPHAIILPNTDGMELLVCYED	1139
ZC4_h.pro	EALSVANEQLFKKILEMWKDIPISSIAFECTORITGWGOKAIEVRSLSQSR	1173
ZC1_h.pro	EGVYVNTYGRITKDVVLQWGEPTSVAYIRSNQIMGWGEKAIETIRSVETG	1189
ZC4_h.pro	VLESELKRRSIIKRLRFLCTRGDKLFESTLRNHHSRVYFMTLGKLEELQS	1223
ZC1_h.pro	HLIDGVFMHKRAQRLLKFLCERNDKVFFASVRSGGSSQVYFMTLGRTSLLSW	1239
ZC4_h.pro	NYDV	1227
ZC1_h.pro		1239

BOX RESIDUES THAT MATCH ZC4_h.pro EXACTLY.

Fig. 14C

Db = LOK1_m

Qy = GEK2_h

Db 1 MAFANFRRI LSTFEKRSREYEHVRRDLDPNDVWEIVGELGDGAFGKVKYKAKNKETGA 60
Qy 1 MAFANFRRI LSTFEKRSREYEHVRRDLDPNEVWEIVGELGDGAFGKVKYKAKNKETGA 60

Db 61 LAAAKVIETKSEEELEDYIVEIEILATCDHPYIVKLLGAYYDGGKLVIMIEFCPPGGAVDA 120
Qy 61 LAAAKVIETKSEEELEDYIVEIEILATCDHPYIVKLLGAYYHDGKLVIMIEFCPPGGAVDA 120

Db 121 IMLELDRGLTEPQIQVVCRCQMLEALNFLHGKRRIIHRDLKAGNVLMTLEGDIRLADFGVSA 180
Qy 121 IMLELDRGLTEPQIQVVCRCQMLEALNFLHRSKRRIIHRDLKAGNVLMTLEGDIRLADFGVSA 180

Db 181 KNLKTLQKRDSFIGTPYWMapevVLCETMKDAPYDYKADIWSLGITLIEMAQIEPPHHEL 240
Qy 181 KNLKTLQKRDSFIGTPYWMapevVLCETMKDTPDYKADIWSLGITLIEMAQIEPPHHEL 240

Db 241 NPMRVLLKIAKSDPPTLLTPSKWSVEFRDFLKIALDKNPETRPSAAQLLQHPFVSRVTSN 300
Qy 241 NPMRVLLKIAKSDPPTLLTPSKWSVEFRDFLKIALDKNPETRPSAAQLLEHPFVSSITSN 300

Db 301 KALRELVAEAKAEVMEEIEDGREDEGEEDAVDAPPLVNHTQDSANVTQPSLDSNKLQD 360
Qy 301 KALRELVAEAKAEVMEEIEDGREDEGEEDAVDAASTLENHTQNSSEVSPPSLNADKPLEE 360

Fig. 15A

* * * * *
Db 361 S-STPLPPSQPEPVNGPCSPSGDGPLQTTSPADGLSKNDNDLKVPVPLRKSRPLSMDA 419
Qy 361 SPSTPLAPSQSQDSVNEPCSPSGDRSLQTTSPVAVPVGNGENGLAVPVLKSRPVSMMDA 420

* * * * *
Db 420 RIQMDEEKQIPDQDENPSPAASKSQKANQSRPNSSALETLGGEALTNGGLELPSSVTPSH 479
Qy 421 RIQVAQEKQVAEQGGDLSPAANRSQKASQSRPNSSALETLGGEKLANGSLEPPAQAAPGP 480

* * * * *
Db 480 SKRASDCSNLSTSESM DYGTSLADLSLNKETGSLSLKGSKLHNKTLKRTRRFVVDGVEV 539
Qy 481 SKRSDCSSLCTSESM DYGTNLSTDLSLNKEMGSLSIKDPKLYKTKLKRTRKFVVDGVEV 540

* * * * *
Db 540 SITTSKIISEDEKKDEEMRFLRRQELRELRLQKEEHRNQTQLSSKHLEQLQEMHKRFEQ 599
Qy 541 SITTSKIISEDEKKDEEMRFLRRQELRELRLQKEEHRNQTQLSNKHLEQLQEMHKRFEQ 600

* * * * *
Db 600 EINAKKKFYDVELENLERQKQKQVEKMEQDHSVRRKEEAKRIRLEQDRDYAKFQEQLKQM 659
Qy 601 EINAKKKFFDTELENLERQKQKQVEKMEQDHA VRRREEARIRLEQDRDYTRFQEQLKLM 660

* * * * *
Db 660 KKEVKSEVEKLPRQQRKESMKQKMEEHSQKKQLDRDFVAKQKEDLELAMRKLTTENRRE 719
Qy 661 KKEVKNEVEKLPRQQRKESMKQKMEEHTQKKQLDRDFVAKQKEDLELAMKRLTTDNRRRE 720

```

*****
Db 720 ICDKERDCLSKKQELLRDREAALWEMEEHQLQERHQLVKQQLKDQYFLQRHDLRLKKHEKE 779
Qy 721 ICDKERECLMKKQELLRDREAALWEMEEHQLQERHQLVKQQLKDQYFLQRHELRLKKHEKE 780

*****
Db 780 REQMQRYNQRMMEQLKVRQQQEKAARLPKIQRSDGETRMAMYKKSLHINGAGSASEQREKI 839
Qy 781 REQMQRYNQRMIEQLKVRQQQEKAARLPKIQRSEGKTRMAMYKKSLHINGGSAAEQREKI 840

*****
Db 840 KQFSQQ'E EKQRQKAERLQQQKKHEHQMRDMVAQCESNMSELQQQLQNEKCYLLVEHETQKLK 899
Qy 841 KQFSQQ'E EKQRQKSERLQQQKKHENQMRDMLAQCESNMSELQQQLQNEKCHLLVEHETQKLK 900

*****
Db 900 ALDESHNQSLKEWRDKLRPRKKALEEDLNQKKREQEMFFKLSEEA-PRPTTPSKASNFF 958
Qy 901 ALDESHNQNLKEWRDKLRPRKKALEEDLNQKKREQEMFFKLSEEAECNPSTPSKAAKFF 960

*****
Db 959 PYSSGDAS 966
Qy 961 PYSSGDAS 968
```

Fig. 15C